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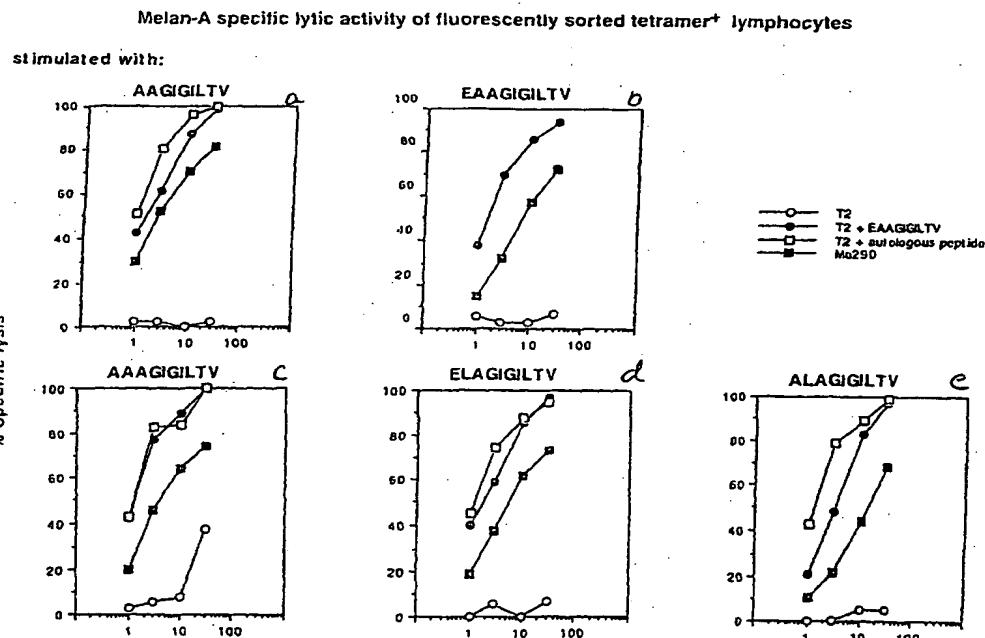
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(54) Title: ISOLATED NONA AND DECAPEPTIDES WHICH BIND TO HLA MOLECULES, AND THE USE THEREOF



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(57) Abstract: Recombinant vectors which produce tumor rejection antigen precursors and tumor rejection antigens are disclosed, as well as the uses of these.

**ISOLATED NONA AND DECAPEPTIDES WHICH
BIND TO HLA MOLECULES, AND THE USE THEREOF**

RELATED APPLICATION

This is a continuation in part of Serial No. 09/099,543, filed June 18, 1998, which is a continuation-in-part of Serial No. 09/061,388, filed January 13, 1998, which is a continuation in part of Serial No. 08/880,963, filed June 23, 1997, incorporated by reference. A portion of the invention was published by the inventors, less than one year before the filing date of the first continuation-in-part application. See Romero et al., *J. Immunol.* 159:2366 (1997) incorporated by reference.

FIELD OF THE INVENTION

This invention relates to peptides which are useful in the context of cellular immunology. More particularly, the invention relates to peptides which bind to HLA molecules on the surface of cells, as well as recombinant constructs for making these peptides. At least some of these peptides also induce the activation of cytolytic T cells, when they are complexed with their partner HLA molecule. Also a part of the invention are the uses of these peptides in areas such as identifying HLA-A2 positive cells, provoking T cells, determining presence of particular T cells, as well as cytolytic T cells themselves.

BACKGROUND AND PRIOR ART

The study of the recognition or lack of recognition of cancer cells by a host organism has proceeded in many different directions. Understanding of the field presumes some understanding of both basic immunology and oncology.

Early research on mouse tumors revealed that these displayed molecules which led to rejection of tumor cells when transplanted into syngeneic animals. These molecules are "recognized" by T-cells in the recipient animal, and provoke a cytolytic T-cell response with lysis of the transplanted cells. This evidence was first obtained with tumors induced *in vitro* by chemical carcinogens, such as methylcholanthrene. The antigens expressed by the tumors and which elicited the T-cell response were found to be different for each tumor. See Prehn, et al., *J. Natl. Canc. Inst.* 18:769-778 (1957); Klein et al., *Cancer Res.* 20:1561-1572 (1960); Gross, *Cancer Res.* 3:326-333 (1943), Basombrio, *Cancer Res.* 30:2458-2462 (1970) for general

teachings on inducing tumors with chemical carcinogens and differences in cell surface antigens. This class of antigens has come to be known as "tumor specific transplantation antigens" or "TSTAs." Following the observation of the presentation of such antigens when induced by chemical carcinogens, similar results were obtained when tumors were induced in vitro via ultraviolet radiation. See Kripke, J. Natl. Canc. Inst. 53:333-1336 (1974).

While T-cell mediated immune responses were observed for the types of tumor described supra, spontaneous tumors were thought to be generally non-immunogenic. These were therefore believed not to present antigens which provoked a response to the tumor in the tumor carrying subject. See Hewitt, et al., Brit. J. Cancer 33:241-259 (1976).

The family of tum⁺ antigen presenting cell lines are immunogenic variants obtained by mutagenesis of mouse tumor cells or cell lines, as described by Boon et al., J. Exp. Med. 152:1184-1193 (1980), the disclosure of which is incorporated by reference. To elaborate, tum⁺ antigens are obtained by mutating tumor cells which do not generate an immune response in syngeneic mice and will form tumors (i.e., "tum⁺" cells). When these tum⁺ cells are mutagenized, they are rejected by syngeneic mice, and fail to form tumors (thus "tum⁻"). See Boon et al., Proc. Natl. Acad. Sci. USA 74:272 (1977), the disclosure of which is incorporated by reference. Many tumor types have been shown to exhibit this phenomenon. See, e.g., Frost et al., Cancer Res. 43:125 (1983).

It appears that tum⁺ variants fail to form progressive tumors because they initiate an immune rejection process. The evidence in favor of this hypothesis includes the ability of "tum⁻" variants of tumors, i.e., those which do not normally form tumors, to do so in mice with immune systems suppressed by sublethal irradiation, Van Pel et al., Proc. Natl. Acad. Sci. USA 76:5282-5285 (1979); and the observation that intraperitoneally injected tum⁺ cells of mastocytoma P815 multiply exponentially for 12-15 days, and then are eliminated in only a few days in the midst of an influx of lymphocytes and macrophages (Uyttenhove et al., J. Exp. Med. 152:1175-1183 (1980)). Further evidence includes the observation that mice acquire an immune memory which permits them to resist subsequent challenge to the same tum⁺ variant, even when immunosuppressive amounts of radiation are administered with the following challenge of cells (Boon et al., Proc. Natl. Acad. Sci. USA 74:272-275 (1977); Van Pel et al., supra; Uyttenhove et al., supra). Later research found that when spontaneous tumors were subjected to mutagenesis,

immunogenic variants were produced which did generate a response. Indeed, these variants were able to elicit an immune protective response against the original tumor. See Van Pel et al., J. Exp. Med. 157:1992-2001 (1983). Thus, it has been shown that it is possible to elicit presentation of a so-called "tumor rejection antigen" in a tumor which is a target for a syngeneic rejection response. Similar results have been obtained when foreign genes have been transfected into spontaneous tumors. See Fearon et al., Cancer Res. 48:2975-1980 (1988) in this regard.

A class of antigens has been recognized which are presented on the surface of tumor cells and are recognized by cytolytic T cells, leading to lysis. This class of antigens will be referred to as "tumor rejection antigens" or "TRAs" hereafter. TRAs may be the result of naturally occurring, intracellular processes, may be synthetically produced peptides identical to naturally occurring TRAs (i.e., those produced via intracellular processing), or may be "artificial" peptides which are not identical to naturally processed TRA peptides, but are designed to enhance binding to an MHC molecule, and/or the ability of CTLs to proliferate and exert effector function upon recognition of the complexes produced when the peptide binds to the MHC molecule. Synthetic TRAs may differ in one or more of their amino acids relative to naturally occurring TRAs via replacement, deletion, and/or addition of amino acids as long as required anchor binding residues are present, and/or may be modified via modification of side chains on the amino acids of the peptide. Similarly, "tumor rejection antigen precursors" can refer to naturally occurring molecules which are processed in the manner described supra, as well as molecules which differ from naturally occurring tumor rejection antigen precursors in their amino acid sequence via additions, deletions, and/or modifications as described supra, but which are processed to one or more naturally occurring and/or synthetic tumor rejection antigens, such as are described, supra. TRAs may or may not elicit antibody responses. The extent to which these antigens have been studied, has been via cytolytic T cell characterization studies, in vitro, i.e., the study of the identification of the antigen by a particular cytolytic T cell ("CTL" hereafter) subset. The subset proliferates upon recognition of the presented tumor rejection antigen, and the cells presenting the tumor rejection antigens are lysed. Characterization studies have identified CTL clones which specifically lyse cells expressing the tumor rejection antigens. Examples of this work may be found in Levy et al., Adv. Cancer Res. 24:1-59 (1977); Boon et al., J. Exp. Med. 152:1184-1193 (1980); Brunner et al., J. Immunol. 124:1627-1634 (1980); Maryanski et al., Eur. J.

Immunol. 124:1627-1634 (1980); Maryanski et al., Eur. J. Immunol. 12:406-412 (1982); Palladino et al., Cancer Res. 47:5074-5079 (1987). This type of analysis is required for other types of antigens recognized by CTLs, including minor histocompatibility antigens, the male specific H-Y antigens, and the class of antigens referred to as "tum-" antigens, and discussed herein.

A tumor exemplary of the subject matter described supra is known as P815. See DePlaen et al., Proc. Natl. Acad. Sci. USA 85:2274-2278 (1988); Szikora et al., EMBO J 9:1041-1050 (1990), and Sibille et al., J. Exp. Med. 172:35-45 (1990), the disclosures of which are incorporated by reference. The P815 tumor is a mastocytoma, induced in a DBA/2 mouse with methylcholanthrene and cultured as both an in vitro tumor and a cell line. The P815 line has generated many tum⁻ variants following mutagenesis, including variants referred to as P91A (DePlaen, supra), 35B (Szikora, supra), and P198 (Sibille, supra). In contrast to tumor rejection antigens - and this is a key distinction - the tum⁻ antigens are only present after the tumor cells are mutagenized. Tumor rejection antigens are present on cells of a given tumor without mutagenesis. Hence, with reference to the literature, a cell line can be tum⁺, such as the line referred to as "P1," and can be provoked to produce tum⁻ variants. Since the tum⁻ phenotype differs from that of the parent cell line, one expects a difference in the DNA of tum⁻ cell lines as compared to their tum⁺ parental lines, and this difference can be exploited to locate the gene of interest in tum⁻ cells. As a result, it was found that genes of tum⁻ variants such as P91A, 35B and P198 differ from their normal alleles by point mutations in the coding regions of the gene. See Szikora and Sibille, supra, and Lurquin et al., Cell 58:293-303 (1989). This has proved not to be the case with the TRAs of this invention. These papers also demonstrated that peptides derived from the tum⁻ antigen are presented by H-2^d Class I molecules for recognition by CTLs. P91A is presented by L^d, P35 by D^d and P198 by K^d.

PCT application PCT/US92/04354, filed on May 22, 1992 assigned to the same assignee as the subject application, teaches a family of human tumor rejection antigen precursor coding genes, referred to as the MAGE family. Several of these genes are also discussed in van der Bruggen et al., Science 254:1643 (1991). It is now clear that the various genes of the MAGE family are expressed in tumor cells, and can serve as markers for the diagnosis of such tumors, as well as for other purposes discussed therein. See also Traversari et al., Immunogenetics

35:145 (1992); van der Bruggen et al., Science 254:1643 (1991) and De Plaen, et al., Immunogenetics 40:360 (1994). The mechanism by which a protein is processed and presented on a cell surface has now been fairly well documented. A cursory review of the development of the field may be found in Barinaga, "Getting Some 'Backbone': How MHC Binds Peptides," 5 Science 257:880 (1992); also, see Fremont et al., Science 257:919 (1992); Matsumura et al., Science 257:927 (1992); Engelhard, Ann. Rev. Immunol. 12:181-207 (1994); Madden, et al., Cell 75:693-708 (1993); Ramensee, et al., Ann. Rev. Immunol. 11:213-244 (1993); Germain, Cell 76:287-299 (1994). These papers generally point to a requirement that the peptide which binds to an MHC/HLA molecule be nine amino acids long (a "nonapeptide"), and to the importance of the second and ninth residues of the nonapeptide. For H-2K^b, the anchor residues are positions 5 and 8 of an octamer, for H-2D^b, they are positions 5 and 9 of a nonapeptide while the anchor residues for HLA-A1 are positions 3 and 9 of a nonamer. Generally, for HLA molecules, positions 2 and 9 are anchors.

10 Studies on the MAGE family of genes have now revealed that a particular nonapeptide is in fact presented on the surface of some tumor cells, and that the presentation of the nonapeptide requires that the presenting molecule be HLA-A1. Complexes of the MAGE-1 tumor rejection antigen (the "TRA" or "nonapeptide") leads to lysis of the cell presenting it by cytolytic T cells ("CTLs").

15 Research presented in, e.g., U.S. Patent No. 5,405,940 filed August 31, 1992, found that when comparing homologous regions of various MAGE genes to the region of the MAGE-1 gene coding for the relevant nonapeptide, there is a great deal of homology. Indeed, these observations lead to one of the aspects of the invention disclosed and claimed therein, which is a family of nonapeptides all of which have the same N-terminal and C-terminal amino acids. These nonapeptides were described as being useful for various purposes which includes their use 20 as immunogens, either alone or coupled to carrier peptides. Nonapeptides are of sufficient size to constitute an antigenic epitope, and the antibodies generated thereto were described as being useful for identifying the nonapeptide, either as it exists alone, or as part of a larger polypeptide.

25 The preceding survey of the relevant literature shows that various peptides, usually eight, nine, or ten amino acids in length, complex with MHC molecules and present targets for recognition by cytolytic T cells. A great deal of study has been carried out on melanoma, and

melanoma antigens which are recognized by cytolytic T cells are now divided into three broad categories. The first, which includes many of the antigens discussed, supra, (e.g., MAGE), are expressed in some melanomas, as well as other tumor types, and normal testis and placenta. The antigens are the expression product of normal genes which are usually silent in normal tissues.

A second family of melanoma antigens includes antigens which are derived from mutant forms of normal proteins. Examples of this family are MUM-1 (Coulie, et al., Proc. Natl. Acad. Sci. USA 92:7976-7980(1995)); CDK4 (Wölfel, et al., Science 269:1281-1284(1995)); β catenin (Robbins, et al., J. Exp. Med. 183:1185-1192 (1996)); and HLA-A2 (Brandel, et al., J. Exp. Med. 183:2501-2508 (1996)). A third category, also discussed, supra, includes the differentiation antigens which are expressed by both melanoma and melanocytes. Exemplary are tyrosinase, gp100, gp75, and Melan A/Mart-1. See U.S. Patent No. 5,620,886 incorporated by reference, with respect to Melan-A. See Wölfel, et al., Eur. J. Immunol. 24:759 (1994) and Brichard, et al., Eur. J. Immunol. 26:224 (1996) for tyrosinase; Kang, et al., J. Immunol. 155:1343 (1995); Cox, et al., Science 264:716 (1994); Kawakami, et al., J. Immunol. 154:3961 (1995) for gp 100; Wang, et al., J. Exp. Med. 183:1131 (1996) for gp 75.

Cytolytic T cells ("CTLs" hereafter) have been identified in peripheral blood lymphocytes and tumor infiltrating lymphocytes, of melanoma patients who are HLA-A*0201 positive. See Kawakami, et al. Proc. Natl. Acad. Sci. USA 91:3515 (1994); Coulie, et al., J. Exp. Med. 180:35 (1994). When ten HLA-A*0201 restricted Melan-A specific CTLs derived from different patients were tested, nine of them were found to recognize and react with the peptide Ala Ala Gly Ile Gly Ile Leu Thr Val, (SEQ ID NO: 2), which consists of amino acids 27-35 of Melan-A. (Kawakami, et al., J. Exp. Med. 180:347-352 (1994)). Rivoltini, et al., J. Immunol. 154:2257 (1995), showed that Melan-A specific CTLs could be induced by stimulating PBLs from HLA-A*0201 positive normal donors, and melanoma patients, using SEQ ID NO: 2. The strength of this response has led to SEQ ID NO: 2 being proposed as a target for vaccine development. It has now been found, however, that a decapeptide, i.e.,

Glu Ala Ala Gly Ile Gly Ile Leu Thr Val

(SEQ ID NO: 1), is actually a better target than SEQ ID NO: 2. This recognition has led to work set forth herein, which is part of the invention.

The majority of peptides which have been identified as binding to HLA-A*0201 are 9 or 10 amino acids in length, and are characterized by two anchor residues. The first is Leu or Met at position 2, and the second is Leu or Val at position 9. See Falk, et al., *Nature* 351:290 (1991). Ruppert, et al., in *Cell* 74:929 (1993), show that amino acids found at other positions within a nona-or decapeptide may also have a role in the peptide -HLA-A*0201 interaction. They show, e.g., that a negatively charged residue or proline at position 1 was associated with poor HLA-A*0201 binding.

5

What is interesting about this work is that the two peptides represented by SEQ ID NOS: 1 and 2 do not possess the major anchor residue at position 2 and, the strong binder SEQ ID NO: 10 1 has a negatively charged residue at position 1.

10

A strong binder is not necessarily a stable binder, meaning that the interaction between peptide and HLA molecule may be, and is, brief. When it is desired to induce CTLs, to identify them or to carry out other types of experiments, it would be desirable to have a peptide with the ability to bind to an MHC Class I molecule which binds with high affinity and forms stable complexes. See Van der Burg et al., *J. Immunol.*, 156:3308 (1996).

15

The invention involves, inter alia, the development of new nonamers and decamers which are surprisingly good HLA binders and CTL stimulators. These molecules, as well as their uses, are among the features of the invention which are set forth in the disclosure which follows.

BRIEF DESCRIPTION OF THE FIGURES

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Figure 1 shows results of experiments carried out to determine if tumor infiltrating lymphocyte populations would lyse cells presenting complexes of HLA-A*0201 and various peptides on their surfaces.

Figures 2a - 2d show stability studies comparing various peptides.

Figure 3 shows antigenic activity of various peptides when tested with TILNs.

25

Figure 4 parallels figure 3, but uses CTLs generated from PBLs by stimulation with various peptides.

Figures 5a - 5r show results of flow cytometry studies, following stimulation of PBMCs with various peptides.

Figures 6a - 6e depict results of lytic activity assays on PBMCs which have been stimulated with various peptides.

Figures 7a - 7e present data on Melan-A specific lytic activity of fluorescently sorted lymphocytes positive for tetramers containing SEQ ID NO: 1, following stimulation with other peptides.

Figure 8 shows quantitative assessment of peptide dependent lytic activity of a Melan-A monospecific CTL line.

Figures 9A and 9B show that cells transfected with vaccinia virus construct of the invention stimulate T cell proliferation and lysis of target cells.

10

DETAILED DESCRIPTION OF PREFERRED EMBODIMENTS

EXAMPLE 1

In these experiments tumor infiltrating lymphocytes ("TILs" hereafter), were generated from tumor invaded lymph nodes of patients who were HLA-A*0201 positive. The experiments were designed so as to avoid antigen specific selection *in vitro*, and the methodology is now set forth.

20

Biopsies of tumor infiltrated lymph nodes ("TILNs" hereafter) were minced to single cell suspensions, and then cultured in 24 well culture plates. A total of 3×10^6 cells were added to 2 mls of Iscove's Dulbecco medium which had been supplemented with Asn (0.24mM), Arg (0.55mM), and Gln (1.5mM), and 10% pooled human A⁺ serum (serum obtained from type A blood donors), together with recombinant human IL-2 (100 u/ml), and IL-7 (10ng/ml). These were the only cytokines used to culture the cell suspensions, so as to avoid antigen specific selection *in vitro*. The suspensions were cultured for 2-3 weeks, and the cells were then characterized for cell surface phenotype. Only populations with greater than 75% CD8⁺T cells, and of desired cytolytic activity were used. This second property was determined by combining the TILN populations with autologous cells, a melanoma cell line previously characterized as being HLA-A*0201 positive (Me290), a melanoma cell line known to be HLA-A*0201 negative (Me260) or cell line T2, which does not process antigen, together with the peptide of SEQ ID NO: 1. The peptide was added at 1 μ M, together with varying ratios of effector (TILN) cells, and the target cells. The results presented in Figure 1, show results obtained using LAU 132 and

LAU 203, two TILN populations identified via this method. In Figure 1, "M10" is SEQ ID NO: 1, and the additional abbreviations are as set forth, supra. The assay was a 4-hour ^{51}Cr release assay, carried out in the absence or presence of exogenously added peptide. In Figure 1, open symbols stand for the absence of the peptide, and solid symbols for its presence. In this assay, the target cells were labelled with ^{51}Cr for one hour, at 37°C, and were then washed two times. Labeled cells (1000 cells in 50 μl) were added to a 50 μl sample of effector cells (varying amounts, as indicated herein), in the presence or absence of 50 μl of antigenic peptide (1 $\mu\text{g}/\text{ml}$). Prior to their addition, the effector cells had been incubated for a minimum of 20 minutes at 37°C, in the presence of unlabelled natural killer (NK) cell targets (50,000 cells per well), in order to eliminate any non-specific lysis due to NK-like effectors present in the effector population. The ^{51}Cr release was measured after 4 hours of incubation at 37°C, and percent specific lysis was calculated as:

$$\frac{100 \times [(\text{experimental release} - \text{spontaneous release})]}{(\text{total release} - \text{spontaneous release})}$$

As Figure 1 shows, the two TILN populations lysed the HLA-A*0201 positive cell line equally well, whether or not the peptide was added. The HLA-A*0201 negative line, Me260, was not lysed in either situation, and T2, which does not process antigen, was lysed only when the peptide was added. These results show that the two TILN populations used hereafter recognize the epitope defined by SEQ ID NO: 1, when complexed to HLA-A*0201 positive cells.

EXAMPLE 2

The experiments described, supra, were modified somewhat, to determine if the TILNs recognized other peptides better than SEQ ID NO: 1. In these experiments, the following peptides were synthesized, using known methods:

Ala Ala Gly Ile Gly Leu Thr Val (SEQ ID NO: 2)

Ala Ala Gly Ile Gly Ile Leu Thr Val Ile (SEQ ID NO: 3)

Ile Leu Thr Val Ile Leu Gly Val Leu (SEQ ID NO: 4)

These peptides correspond, respectively, to amino acids 27-35, 27-36, and 32-40 of Melan-A.

TILN recognition was determined by incubating T2 cells (target), with TILNs (effector), at an effector: target ratio of 30:1. Varying concentrations of the peptides SEQ ID NOS: 1, 2, 3, or 4 were used. The ^{51}Cr release assay discussed, supra, was used. The following Table sets forth the results of these experiments, wherein the peptide concentration is that which gave 50% of maximum activity. Relative activity is that obtained via comparison to SEQ ID NO: 2, i.e.,: [nM]50%[SEQ ID NO: 2]/[nM]50% [test peptide].

TABLE I

Peptide Sequence	TILN LAU 203		TILN LAU 132	
	Peptide [nM] 50%	Relative activity	Peptide [nM] 50%	Relative activity
AAGIGILTV ₂₇₋₃₅	40	1	15	1
EAAGIGILTV ₂₆₋₃₅	1.5	27	1	15
AAGIGILTVI ₂₇₋₃₆	600	0.06	300	0.05
ILTVILGV ₃₂₋₄₀	>10 ⁴	<4 x 10 ⁻³	>10 ⁴	<1.5 x 10 ⁻³

It will be seen that SEQ ID NO: 1 had significantly higher activity than the other peptides tested.

EXAMPLE 3

As was pointed out, supra, the decapeptide of SEQ ID NO: 1 had a higher efficiency of recognition than the nonamer of SEQ ID NO: 2. Experiments were carried out to determine if this was the result of better binding of the peptide of SEQ ID NO: 1 to HLA-A*0201 molecules. These involved a functional peptide competition assay. This type of assay is described by Gaugler et al., *J. Exp. Med.* 174:921 (1994), incorporated by reference, but is described herein. In this assay, HLA-A*0201 expressing target cells (T2 cells) were labelled with ^{51}Cr and then incubated, for 15 minutes, with varying concentrations of peptides. A suboptimum concentration of mutant Ras 5-14 peptide was added. This peptide has amino acid sequence:

Lys Leu Val Val Val Gly Ala Val Gly Val (SEQ ID NO: 5).

After 15 minutes a sample of CTL clone 7 RAS was added. This CTL clone had been obtained from the draining lymph node of an HLA-A*0201 human/β-microglobulin double transgenic mouse that had been injected with the peptide of SEQ ID NO: 20. The CTLs were added at a ratio of 5 lymphocytes (10,000 cells/well):1 target cell. The cells were incubated at 37°C for four hours, and then the assay was terminated. In addition to the peptide of SEQ ID NO: 1, those of SEQ ID NO: 2, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 3, SEQ ID NO: 4, and SEQ ID NO: 8:

Tyr Ala Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 6)

Phe Ala Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 7)

Glu Ala Asp Pro Thr Gly His Ser Thr (SEQ ID NO: 8)

were tested. SEQ ID NO: 6 is a known peptide, derived from MAGE-1, which is known to bind to HLA-A1 molecules and stimulate lysis. See U.S. Patent No. 5,405,940, SEQ ID NO: 12, incorporated by reference.

When SEQ ID NO: 5 was used alone, the lysis percentage was 80%. Control lysis, with no peptide, was 4%:

The results indicated that SEQ ID NO: 1 showed five fold more efficient binding than SEQ ID NO: 2. Both SEQ ID NOS: 3 and 4 bound with activities comparable to SEQ ID NO: 2, while the control (SEQ ID NO: 8), showed no binding. Both of SEQ ID NOS: 6 and 7 showed significantly improved binding as compared to SEQ ID NO: 2. Similar results were obtained when a human CTL clone, specific for a complex of HLA-A*0201 and a different peptide, was used. The table which follows presents relative competitor activity as concentration of SEQ ID NO: 2 required to inhibit control lysis by 50%, divided by concentration of peptide being tested to secure the same result:

Table II
Relative Competitor Activity

Peptide	Exp1	Exp2	Exp3
SEQ ID NO: 2	1	1	1
SEQ ID NO: 1	4	4	5
SEQ ID NO: 7	12	17	20
SEQ ID NO: 6	8	10	10
SEQ ID NO: 3	Not Done	Not Done	2
SEQ ID NO: 4	Not Done	Not Done	2

EXAMPLE 4

Relative HLA-A*0201 peptide binding activity was then determined in another assay, based upon a flow cytometric assay. In these experiments, 2×10^5 T2 cells were incubated with varying concentrations of the peptides of SEQ ID NOS: 1, 2, 4, 6, or 7, for 16 hours, at 23°C , in the presence of 2 ug/ml of human β_2 microglobulin. Cells were washed, at 4°C , and then stained with monoclonal antibody BB7.2, labelled with FITC. This mAb is specific for a conformation dependent epitope on HLA-A2 molecules. Fluorescence index was then calculated, by using the formula (mean fluorescence of sample - mean fluorescence of background)/(mean fluorescence of background). See Nijman et al., *Eur. J. Immunol.* 23:1215 (1993). Again, SEQ ID NO: 1 showed highest efficiency of binding (about 10 fold) than SEQ ID NO: 2. SEQ ID NO: 4 showed relative binding activity about the same as SEQ ID NO: 2, while SEQ ID NOS: 6 and 7 had binding activities comparable to SEQ ID NO: 1.

EXAMPLE 5

In these experiments, efficiency of peptide recognition was assessed with a panel of 13 CTL clones, all of which were specific for complexes of HLA-A*0201 and SEQ ID NO: 2.

The same type of ^{51}Cr release assay as is described in, e.g., example 3, supra was carried out. Specifically, T2 cells were labelled with ^{51}Cr (the sodium salt was used), in Tris-Dulbecco buffer, supplemented with 2 mg/ml bovine serum albumin, and a 1:40 dilution of W6/32 ascites as described by Gaugler et al., supra. This stabilizes the MHC molecule. The labelled cells were

added to varying concentrations of peptides, and in varying amounts so as to create differing effector:target ratios. Ten of the thirteen CTL clones tested recognized the decapeptide of SEQ ID NO: 1 more efficiently than the nonapeptide of SEQ ID NO: 2, requiring concentrations of anywhere from 20 to more than 1000 fold lower than the nonapeptide to achieve half-maximal lysis. The three remaining CTLs yielded titration curves which were similar. None of the CTLs 5 recognized complexes of SEQ ID NO: 3 and HLA-A2. In additional experiments, one of the CTL clones was tested in IL-2 release assays, with SEQ ID NO: 1 again proving to be 10 fold more efficient than SEQ ID NO: 2.

EXAMPLE 6

10 A series of peptides were then synthesized, in order to attempt to determine peptides with enhanced binding to HLA-A*0201 molecules. The peptides synthesized are considered to be derivatives of SEQ ID NO: 2 (i.e., Ala Ala Gly Ile Gly Ile Leu Thr Val), and are, in addition to SEQ ID NOS: 6 and 7:

15 Ala Leu Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 9)

Ala Met Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 10)

Leu Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 11)

and

Met Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 12)

For SEQ ID NO: 1, i.e., Glu Ala Ala Gly Ile Leu Thr Val the derivatives were:

20 Glu Leu Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 13)

Glu Met Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 14)

Glu Ala Leu Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 15)

Glu Ala Met Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 16)

Ala Ala Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 17)

25 and

Ala Leu Ala Gly Ile Gly Ile Leu Thr Val (SEQ ID NO: 18)

Three other control peptides were used, i.e.:

Gly Ile Leu Gly Phe Val Phe Thr Leu (SEQ ID NO: 19)

Glu Val Asp Pro Ile Gly His Leu Tyr (SEQ ID NO: 20) and

Phe Leu Trp Gly Pro Arg Ala Leu Val (SEQ ID NO: 21).

SEQ ID NOS: 19 and 20 correspond to amino acids 58-66 of Influenza A matrix protein ("FLUMA"), and amino acids 168-176 of MAGE-3 TRAP, respectively.

In these experiments a peptide known to bind to HLA-A*0201 was used, i.e., amino acids 271-279 of the MAGE-3 TRAP (SEQ ID NO: 21), in an inhibition assay, together with cytolytic T cell line 198NS (Valmori, et al., Canc. Res. 57:735 (1997) which recognizes complexes of SEQ ID NO: 21 and HLA-A*0201. In these assays, varying concentrations of test peptides (1 μ M to 100 μ M) were incubated with ^{51}Cr labelled T2 cells (1000 cells/well), for 15 minutes, at room temperature. A suboptimal dose of SEQ ID NO: 21 was then added (1nM), together with CTL 198NS, in an amount sufficient to create a 5/1 effector/target ratio. A ^{51}Cr release assay was then carried out, in accordance with the method set forth, supra. The amount of test peptide needed to inhibit recognition of complexes by the CTL was calculated, and then binding affinity of each peptide, relative to SEQ ID NO: 2, was calculated, using the formula:

$$R = \frac{\text{ID}_{50}(\text{SEQ ID NO: 2})}{\text{ID}_{50}(\text{test peptide})}$$

If R is greater than one, then the tested peptide bound to HLA-A*0201 with greater affinity than SEQ ID NO: 2. A value less than one indicates lower affinity. The results are set forth below:

TABLE III

Peptide	Sequence	Competitor [μM] 50%	Relative competitor activity
5 Melan-A ₂₇₋₃₅	AAGIGILTV	60	1
	ALGIGILTV	1.5	40
	AMGIGILTV	2	30
	LAGIGILTV	65	1
	MAGIGILTV	55	1
10 Melan-A ₂₆₋₃₅	EAAGIGILTV	15	4
	ELAGIGILTV	6.5	9
	EMAGIGILTV	20	3
	EALGIGILTV	100	0.6
	EAMGIGILTV	100	0.6
15 Influenza A matrix ₅₈₋₆₆	YAAGIGILTV	4	15
	FAAGIGILTV	2	30
20 MAGE-3 ₁₆₈₋₁₇₆	GILGFVFTL	1	60
	EVDPIGHLY	>100	<0.6

SEQ ID NOS: 1, 6, 7, 9, 10, 13 and 14 all showed higher affinity than SEQ ID NO: 2.

EXAMPLE 7

One concern in developing MHC binding peptides is that the resulting complexes of MHC molecule and peptide be stable, preferably more stable than the peptide originally found complexed to the MHC molecule.

To test stability of the newly synthesized peptides, T2 cells were incubated, overnight, at room temperature in serum free medium with saturating amounts of peptide (10μM), and 3μg/ml β-microglobulin, to facilitate the assembly of the requisite MHC molecules. Peptides

were then removed, and 10^{-4} M emetine (which inhibits protein synthesis) was added. The cells were then incubated at 37°C for varying periods of time. Aliquots of cells were stained, at various points of the incubation, with a labelled HLA-A2 specific mAb to measure HLA-A2 expression.

5 Stability was determined by comparison with complexes involving SEQ ID NO: 19 which were stable over a 6-hour period. The results are presented in Figures 2A - D. Figure 2A shows mean fluorescence intensity for each peptide. "NC" refers to HLA-A*0201, presented by T2 cells, in the absence of exogenous peptide, while "FLUMA" is SEQ ID NO: 19, and is an acronym for "Flu matrix antigen." In Figure 2A, the peptides are SEQ ID NOS: 2, 1, and 13. In Figure 2B, they are SEQ ID NOS: 2, 9, 10, 11, 12, and 19 ("FLUMA"). In Figure 2C, they are SEQ ID NOS: 1, 13, 14, 15, 16, and 19. In Figure 2D, they are SEQ ID NOS: 1, 6, 7, and 19. The breakup is solely to facilitate the review. Figures 2B-2D show relative complex stability where fluorescent intensities with test peptides were normalized, relative to the stability observed when using SEQ ID NO: 19. SEQ ID NOS: 1 and 2 both form unstable complexes, which decay within one hour. This was also found with SEQ ID NOS: 11 and 12.

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On the other hand, SEQ ID NOS: 6, 7, 13, and 14 formed stable complexes over a 6-hour period, while SEQ ID NOS: 9, 10, 15, 16, formed complexes of intermediate stability.

EXAMPLE 8

20 The antigenic activity of each of the peptides presented, supra, when the peptide was associated with HLA-A*0201, was tested in a ^{51}Cr assay of the type discussed, supra, using TILNs, and CTLs. Dose response analyses were performed on each peptide, and antigenic activity, relative to SEQ ID NO: 2, was calculated. These values are set forth in the following Tables IV and V and figure 3 which present data from TILNs, (Table IV and Figure 3) and CTLs (Table V), respectively.

25 Substituting the N-terminal amino acid of SEQ ID NO: 2 with Leu or Met enhanced activity between 7.5 and 20 fold, while substitutions at the second position nearly abolished it, even though binding to HLA-A* 0201 was increased (Table IV and Figure 3).

SEQ ID NO: 1 was better recognized than SEQ ID NO: 2, and substitution of Ala in the second position of SEQ ID NO: 1 increased recognition 30- and 600 fold, respectively. Such

substitutions at position 3 reduced activity, which was expected. Substitution of position 1 resulted in an increase in recognition.

TABLE IV

5	Peptide Sequence	TILN LAU 203		TILN LAU 132	
		[nM]	Relative activity	[nM]	Relative activity
10	AAGIGILTV	60	1	30	1
	ALGIGILTV	>1000	<0.6	>1000	<0.03
	AMGIGILTV	>1000	<0.6	>1000	<0.03
	LAGIGILTV	6	10	1.5	20
	MAGIGILTV	8	7.5	2.5	12
15	EAAGIGILTV	12	5	3	10
	ELAGIGILTV	2	30	0.05	600
	EMAGIGILTV	2	30	0.05	600
	EALGIGILTV	>1000	<0.06	>1000	<0.03
	EAMGIGILTV	>1000	<0.06	>1000	<0.03
20	YAAGIGILTV	5	20	1	30
	FAAGIGILTV	1	60	0.05	600

The results obtained with CTLs are presented herein. Specifically, five independent HLA-A*0201 restricted Melan-A specific CTL clones were used, each of which is known to lyse melanoma target cells.

The CTLs recognized SEQ ID NO: 2 with varying efficiency. When Leu was used to substitute Ala at position 1, four of the five clones showed enhanced recognition, while similar substitutions at position 2 resulted in a loss of activity. Three of the five clones recognized SEQ ID NO: 1 more efficiently than SEQ ID NO: 2, but all recognized SEQ ID NO: 13 very efficiently, while recognition of SEQ ID NO: 14 resulted in decreased efficiency of recognition to differing degrees, and SEQ ID NO: 15 resulted in reduced recognition for four of five. When SEQ ID NO: 16 was tested, it was surprising that recognition improved, because TIL recognition decreased. With respect to SEQ ID NOS: 16 and 17, there was reduced recognition by the CTLs.

It can be gathered from this that SEQ ID NOS: 11 and 13 were better recognized, consistently, than the other peptides tested, while other peptides were recognized to different degrees.

TABLE V

Peptide sequence	Recognition by clone									
	M77.86		7.10		Mel 1.33		M77.80		1.13	
	Peptide [nM] 50%	Relative activity	Peptide [nM] 50%	Relative activity	Peptide [nM] 50%	Relative activity	Peptide [nM] 50%	Relative activity	Peptide [nM] 50%	Relative activity
AAGIGILTV	15	1	50	1	300	1	300	1	4000	1
ALGIGILTV	90	0.16	>1000	<0.015	>1000	<0.3	>1000	<0.3	>10000	<0.4
AMGIGILTV	>1000	<0.15	>1000	<0.015	>1000	<0.3	>1000	<0.3	>10000	<0.4
LAGIGILTV	0.08	187	1.5	33	150	2	0.03	10000	30	130
MAGIGILTV	0.6	.25	15	3	200	1.5	0.5	600	80	50
EAAGIGILTV	0.15	100	4	12	0.06	5000	600	0.5	2000	2
EALGIGILTV	300	0.05	>1000	<0.015	40	7.5	>1000	<0.3	>10000	<0.4
EAMGIGILTV	0.5	30	1	50	0.02	15000	5	60	50	80
ELAGIGILTV	0.015	1000	0.5	100	0.015	20000	0.5	600	20	200
EMAGIGILTV	550	36	>1000	<0.015	40	7.5	>1000	<0.3	>10000	<0.4
YAAGIGILTV	0.015	1000	35	1.4	>1000	<0.3	1000	0.3	>10000	<0.4
FAAGIGILTV	0.005	3000	7	7	>1000	<0.3	>1000	<0.3	200	20

Additional experiments are depicted in Figure 3 which show recognition of various Melan-A peptide analogues presented by T2 cells, by TILN LAU203 and TILN LAU132. A 4-hour ⁵¹Cr assay was conducted at a lymphocyte to target ration of 30:1.

The first panels of Figure 3 (top and bottom) compare SEQ ID NOS: 2, 9, 10, 11, and 12.

The second set of panels (top and bottom) compare SEQ ID NOS: 1, 13, 14, 15, and 16

The third set (top and bottom) compares SEQ ID NOS: 1, 6 and 7

25

EXAMPLE 9

Based upon the preceding data, the peptide of SEQ ID NO: 13 was used for CTL induction studies.

In accordance with Valmori, et al., supra, peripheral blood lymphocytes from HLA-A*0201 positive melanoma patients were purified by centrifugation, and were enriched for CD3⁺ cells. The enriched subpopulation was then selected for CD8⁺ cells. The resulting subpopulations routinely contained more than 90% CD8⁺ cells, and these were used in further experiments.

The purified, CD8⁺ T cells were plated, at 1-2x10⁶ cells/well, together with 2x10⁶ stimulator cells, the preparation of which is discussed, infra. The effector and stimulator cells were combined in a total of 2ml of Iscove's medium which had been supplemented with 10% human serum, L-arginine (0.55mM), L-asparagine (0.24mM), and L-glutamine (1.5mM), together with recombinant human IL-7 (10ng/ml) and recombinant human IL-2 (10U/ml).

To prepare the stimulator cells, 2x10⁶ autologous PBLs were incubated for 2 hours, at 37°C, in serum free medium, with 20μg/ml of each peptide and 3μg/ml β2-microglobulin. The PBLs were then washed, irradiated, (3000 rads), and then adjusted to an appropriate volume, before being added to the CD8⁺ cell populations. On day 7, cells were restimulated with peptide pulsed, autologous PBLs in complete medium, supplemented with 10ng/ml of recombinant human IL-7, and 10U/ml of recombinant human IL-2. There were weekly restimulations, using PBLs which were peptide pulsed and irradiated. CTL activity was tested for the first time after the second cycle (MC-2).

The results are shown in the following table and in Figure 4. In Figure 4, the source of CD8⁺ cells used was PBLs from patient LAU203. CTL activity was assayed seven days after the second (MC-2) restimulation. Results were obtained using SEQ ID NOS: 1 and 2. These were used to permit comparison to SEQ ID NO: 13.

Note that there was barely any activity in the CD8⁺ cell cultures stimulated with the parental peptides in sample LAU203, while SEQ ID NO: 13 elicited a strong CTL response. This activity was also cross reactive with SEQ ID NO: 1.

The results in the following table describe experiments using the same peptides and using PBL from eight different HLA-A2 positive melanoma patients, LAU203, LAU132, LAU145, LAU86, LAU50, LAU148, LAU161 and LAU119. The most important result obtained herein, however, was the fact that CTLs, induced with SEQ ID NO: 13 did recognize and lyse cells presenting the endogenous peptide.

TABLE VI

		Percentage specific lysis from cultures stimulated with peptide				SEQ ID NO: 1 Melan-A 26-35				SEQ ID NO: 13 Melan-A 26-35 A27L				
tested on		T2	T2 +M10	Me260	Me290	T2	T2 +M10	Me260	Me290	T2	T2 +M10	Me260	Me290	
Patient code	E/T													
5	LAU203	100	38	29	7	17	37	41	15	6	32	83	18	81
		30	29	11	10	0	17	23	7	1	26	96	4	75
		10	3	6	2	0	9	17	0	0	17	73	1	62
	LAU132	100	9	12	1	0	19	19	6	3	34	50	6	31
		30	3	7	2	0	5	10	1	2	16	32	3	28
		10	0	0	5	1	0	0	1	0	5	23	2	7
	LAU145	100	13	24	4	1	39	40	5	9	29	50	6	30
		30	9	12	3	1	15	25	2	1	10	29	5	19
		10	3	6	0	0	4	5	0	0	10	16	3	7
0	LAU86	100	36	29	22	5	44	38	14	10	35	45	24	15
		30	17	15	9	5	20	26	6	0	24	23	10	4
		10	16	5	2	0	10	10	1	0	14	9	1	0
	LAU50	100	21	26	7	5	18	20	5	5	19	26	6	20
		30	7	16	4	5	8	13	1	0	10	18	3	8
		10	7	7	0	4	0	4	1	0	3	12	0	0
	LAU148	100	51	39	13	4	46	45	9	0	34	39	9	4
		30	19	8	5	4	20	26	1	2	19	27	9	3
		10	3	6	1	0	14	14	6	0	13	13	1	0
1	LAU161	100	24	22	6	1	33	31	3	1	25	38	4	23
		30	3	8	6	1	16	12	3	0	18	23	2	13
		10	2	0	5	0	9	7	2	0	5	11	3	4
	LAU119	100	31	27	5	12	33	31	1	4	18	66	5	45
		30	7	13	1	1	17	23	3	4	13	39	4	25
		10	4	0	0	0	9	12	1	0	7	17	2	26
	Clone 6	10	7	75	2	73								
		3	3	74	0	61								
		1	0	63	0	51								

578675.1

EXAMPLE 10

SEQ ID NOS: 1, 6, and 7 were then used to "dissect" the panel of the CTLs described supra. A recognition assay of the type described in example 7, supra, was carried out using these peptides. Four of the CTLs recognized SEQ ID NOS: 1, 6 and 7 equally well. A fifth CTL recognized SEQ ID NOS: 1 and 6, but not SEQ ID NO: 7. Two other CTLs recognized SEQ ID NOS: 1 and 7, but not 6. One CTL only recognized SEQ ID NO: 1.

EXAMPLE 11

A set of experiments were then carried out to study the receptors of the T cells described herein ("TCRs" hereafter), because it is known that different elements combine in the TCR repertoire, forming different TCRs as a result.

To do this, total RNA of 10^6 cells of each CTL clone tested was extracted, following Chomczynski et al., Anal. Biochem. 162:156 (1987). Then, reverse transcription using a poly(dT) primer was carried out, following the instructions in a commercially available product. Following this, aliquots of samples were PCR amplified, using a panel of V α and V β probes, and Ca/C β specific oligonucleotides, in accordance with Genevee, et al., Eur. J. Immunol. 22:1261 (1992), incorporated by reference. Six different V α segments were found, i.e., V α 2, 4, 6, 7, 14, and 21. One clone actually presented two in-frame V α transcripts. Seven different V β segments were found (two clones expressed V β 13, two expressed V β 14, and two expressed V β 16. V β 2, V β 3, V β 7.2 and V β 8.2 were each expressed by one clone).

20

EXAMPLE 12

The determination of the contribution of single amino acid side chains to the interaction between SEQ ID NO: 1 and HLA-A*0201 molecule, was studied, by testing single Ala substituted derivatives. That is to say, derivatives were prepared which were identical to SEQ ID NO: 1 but for a change at position 1, 4, 5, 6, 7, 8, 9, or 10 to Ala.

25

The peptides were prepared, following standard synthetic methods. Then, they were tested in a functional competition assay based upon their ability to inhibit binding of a known HLA-A*0201 binding peptide, i.e.

Tyr Met Asp Gly Thr Met Ser Gln Val (SEQ ID NO: 22),

derived from tyrosinase, and an HLA-A*0201 restricted CTL clone, LAU 132/2. In brief, T2 cells were labelled with ^{51}Cr in the presence of monoclonal antibody W6/32. Both the cells and monoclonal antibody are described supra. Varying concentrations of competitor peptide (50 μl volumes) were incubated with 50 μl of the ^{51}Cr labelled T2 cells (This quantity gives 1000 cells/well) for 15 minutes, at room temperature. Then, 1 nM of the peptide of SEQ ID NO: 22 was added, which is a suboptimal dose, together with 5000 CTLs, per well (a volume of 50 μl). ^{51}Cr release was measured after incubating for four hours at 37°C. The concentration of each competitor peptide required to inhibit ^{51}Cr release by 50% was determined. Comparison was facilitated by calculating relative competitor activity as the concentration of SEQ ID NO: 1 needed for 50% inhibition, divided by the 50% inhibition value for the test peptide.

It was found that substituting Ala for Glu at position 1 (SEQ ID NO: 15) resulted in a 5 fold increase in competitor activity. Substitution of Gly at position 4 or 6 by Ala resulted in decreased activity, of 20 and 10 fold, as did substitution of positions 7 and 10 (about 25 fold, each time). Changes at positions 8 or 9, i.e.

15 Glu Ala Ala Gly Ile Gly Ile Ala Thr Val (SEQ ID NO: 23)

and

Glu Ala Ala Gly Ile Gly Ile Leu Ala Val (SEQ ID NO: 24)

did not result in significant changes in activity.

EXAMPLE 13

20 The stability of complexes formed by the single Ala substitutions of SEQ ID NO: 1, discussed supra, and HLA-A*0201 was then studied. Briefly, T2 cells were loaded with saturating concentrations (10 μM) of the analogs, and incubated overnight at room temperature with the peptide and β 2 microglobulin (3 $\mu\text{g/ml}$), in serum free medium. Excess peptide was removed, and emetine (10^{-4}M) was added to block protein synthesis. Cells were then incubated, 25 for varying time periods, and aliquots were stained with fluorescent labelled anti HLA-A2 monoclonal antibody (BB7.2), to determine the amount of the molecules on the surface. Since the peptide of SEQ ID NO: 19, supra, is known to form stable complexes with HLA-A*0201 (van der Burg, *J. Immunol.* 156:3308 (1996)), this peptide was used as an internal standard. Complex stability was determined by calculating mean fluorescence with analog, subtracting background

fluorescence and dividing by the same values obtained using SEQ ID NO: 9. Background fluorescence was the value obtained using T2 cells treated similarly, but without peptide.

It was found that, over a period of 1-6 hours, complexes of SEQ ID NO: 1/HLA-A'0201 were unstable, and dissociated in less than an hour. SEQ ID NO: 17 formed stable complexes over the same 6-hour period. All other derivatives tested formed complexes with low stability.

EXAMPLE 14

The derivatives described supra were then tested for their relative antigenic activity. In these experiments, two TILN populations, i.e., TILN LAU 132 and TILN LAU 203, preparation of which is described, supra, and a panel of ten different cytolytic T cell lines were tested. Of the ten CTLs, five were derived from infiltrating lymphocytes or tumor infiltrating lymph nodes, and five were from normal donor peripheral blood lymphocytes. All were known to be specific for complexes of HLA-A'0201 and SEQ ID NO: 2; however, given the results discussed supra, showing superiority of SEQ ID NO: 1, this decapeptide was used for comparison.

Antigen recognition was assessed in a ^{51}Cr release assay. Target, T2 cells were labelled with ^{51}Cr for one hour at 37°C , then washed, twice. The labelled target cells (1000 cell samples in 50 ul) were then incubated with varying concentrations of peptides (in 50 ul volume), for 15 minutes at room temperature, before adding effector cells (50 ul). When TILNs were the effector cells, these had been preincubated for at least 20 minutes at 37°C , with unlabelled K562 cells (50,000 cells/well), to eliminate non-specific lysis due to NK-like effectors. The ^{51}Cr was measured in supernatant, harvested after four hours of incubation at 37°C . Percent lysis was determined by subtracting spontaneously released ^{51}Cr from ^{51}Cr released with the tested, divided by a figure obtained by subtracting spontaneous release from total ^{51}Cr , and multiplying the resulting figure by 100. Titration was carried out over concentrations ranging from 10^{-5} to 10^{-13}M . For quantitative comparison, concentrations required for 50% maximal activity, normalized against reference values for SEQ ID NO: 2 were determined.

SEQ ID NO: 17 was found to be recognized 20-60 fold better than the parental decapeptide of SEQ ID NO: 1, by the two TILN populations, in contrast to the other variants tested. With respect to the CTLs, 8 of 10 of those tested recognized the peptide better than they recognized SEQ ID NO: 1 or 2.

Additional differences were observed with respect to the CTL specificity. Five of the ten CTLs tested recognized SEQ ID NO: 1 better than SEQ ID NO: 2. One of these five CTLs recognized SEQ ID NO: 1 efficiently, and SEQ ID NO: 2 poorly. Three of the remaining five clones recognized SEQ ID NOS: 1 and 2 equally efficiently, and two recognized SEQ ID NO: 2 better than SEQ ID NO: 1.

What this shows is a strong degree of diversity in fine specificity of tumor reactive CTLs.

EXAMPLE 15

A further set of experiments were then carried out to determine if diversity of antigenic specificity, as displayed by the CTL clones, supra, was a general characteristic of the T cell repertoire for the antigen SEQ ID NO: 1 or was attributable to different methodologies used to derive the CTLs. To test this, the source of the specific T cells had to be one which had not been subjected to antigen driven selection from in vitro stimulation with peptides. The TILN population LAU 203, described supra, was used. As was shown in the prior examples, the population exhibits relatively high CTL activity against Melan-A HLA-A*0201 positive melanoma cells. CTL clones were derived from this population, by limiting dilution cultures, in the presence of irradiated, allogenic PBMCs, Epstein Barr Virus transformed B lymphocytes, phytohemagglutinin, and recombinant IL-2. Using standard probability models, clones were derived from cultures having probable clonality of higher than 90%. These were then expanded, by plating 5×10^3 cells, every 3-4 weeks, into microtiter plates, together with irradiated feeder cells (5×10^4 allogenic PBMCs, and 2.10^4 EBV transformed B cells), with PHA and recombinant IL-2.

Two independent experiments were carried out, resulting in 130 growing clones. When these were tested in a ^{51}Cr release assay, of the type described supra, 11 of these were found to recognize at least one of SEQ ID NOS: 1 and 2.

In order to determine fine specificity, the type of antigen recognition assay described supra was carried out, using SEQ ID NOS: 1, 2 and 17. It was found that four clones recognized SEQ ID NO: 1 better than SEQ ID NO: 2 (i.e., relative antigenic activity was at least 10 fold greater), six clones recognized the two peptides equally well, and one recognized SEQ ID NO: 2 better than SEQ ID NO: 1. Nine CTLs recognized SEQ ID NO: 17 better than SEQ ID NOS:

1 and 2, with one of the clones actually recognizing SEQ ID NO: 17 at nanomolar concentrations, in contrast to micromolar concentrations for the peptides SEQ ID NO: 1 and SEQ ID NO: 2.

EXAMPLE 1'6

5 The *in vitro* immunogenicity of the peptides of the invention was determined. To do this, PBMCs from LAU 203 (1.0×10^7 cells per test), were stimulated by adding 1 μ M of peptide into the culture medium containing the cells. The peptides tested were those defined by SEQ ID NOS: 1, 2, 13, 17 and 18. The peptide defined by SEQ ID NO: 19 was used as a negative control.

10 Following the addition of the peptides, the cultures were stimulated weekly with autologous PBMCs which had been pulsed for 1 hour with one of the peptides listed supra, at 37°C. In other words, a culture treated with SEQ ID NO: 1 was restimulated by having PBMCs pulsed with SEQ ID NO: 1. The restimulating cells were washed, thoroughly, and irradiated prior to their use.

15 Seven days after stimulation, the cultures were monitored to determine presence of CD8⁺ cells, which were reactive with tetramers of HLA-A2 and SEQ ID NO: 13. This step was repeated a total of three times, over a 3-week period. To make the tetramers, it was first necessary to prepare constructs which would encode modified HLA-A*0201 molecules. To do this, total RNA was extracted from HLA-A*0201 positive cells, and HLA-A*0201 was then cloned, using specific primers for the molecule, and reverse transcription polymerase chain reaction (RT-PCR). Altman et al., Science 274:94-96 (October 4, 1996) incorporated by reference, was followed. Simultaneously with the RT-PCR, the amino terminal nucleotide sequence was altered to optimize protein expression in the vector used. See Garboczi et al., Proc. Natl. Acad. Sci. USA 89:3429 (1992) incorporated by reference. Once this was done, the extracellular coding portion of the molecule was amplified, again using specific primers. The resulting construct was recloned into a vector which would produce a BirA biotinylation recognition site in frame at the 3'-end of the HLA-A*0201 heavy chain. The modified HLA-A*0201 and β 2 microglobulin were overexpressed in separate E. coli cultures. The resulting inclusion bodies were purified and the HLA and β 2 microglobulin recombinant proteins were

solubilized into urea, and then refolded in a refolding solution, at 4°C to form complexes. (The refolding solution contained 100 mM Tris, at pH 8.0, L-arginine, 400 mM, EDTA, 2 mM, reduced glutathione, 5 mM, oxidized glutathione, 0.5 mM, PMSF, 0.1 mM, HLA heavy chain and β 2 microglobulin, 1 μ M, and 10 μ M of the peptide of interest). The refolding solution was concentrated to 7.5 ml, using standard techniques. Then, refolding buffer was exchanged with 5 BirA reaction buffer (Tris 100 mM, pH 7.5, NaCl 200 mM, Mg Cl₂ 5 mM, PMSF 100 μ M, leupeptin 1 μ M, and pepstatin 1 μ M), the last three being added immediately before use.

The complexes were then biotinylated with biotin holoenzyme synthase (the BirA enzyme) by combining the refold mix containing the HLA-A2 complex with 50 μ M enzyme, 100 mM biotin in 200 mM Tris, and 100 mM adenosine triphosphate. The mixture was incubated overnight at room temperature. The biotinylated complexes were then purified, and combined with phycoerythrin-labeled streptavidin, to produce tetrameric structures. These were isolated, and reconstituted in small volumes, at a concentration of 1 mg/ml.

Peptides of SEQ ID NO: 13 were added to bind to the tetramers. The total number of T 10 cells positive for the tetramers relative to the total number of CD8⁺ cells in each sample was determined. These results are shown in Figure 5. The analogues were all found to have induced 15 CD8⁺ cells specific for SEQ ID NO: 13.

EXAMPLE 17

Seven days after the third stimulation cycle, the cultures were tested in a ⁵¹Cr release 20 assay to determine if they could lyse T2 cells in the presence or absence of SEQ ID NO: 1. These assays were carried out essentially as described in example 14, supra. The results are presented in Figure 6. It was found that stimulation with the analogues actually resulted in more vigorous 25 expansion of CD8⁺ cells reactive with the tetramers described supra, than did stimulation with SEQ ID NO: 1 or SEQ ID NO: 2. Further, the Melan-A specific lysis correlated directly with the percentage of the CD8⁺ cells which were also tetramer specific, suggesting comparable lytic capacity.

EXAMPLE 18

A further set of experiments were carried out to study the antigen specificity of CD8⁺, tetramer positive cells. To do this, the CD8⁺ tetramer positive cells were purified from each culture using standard flow cytometry sorting methods. The cells were then expanded in vitro, using standard mitogen stimulation techniques. They were then tested for their lytic activity on T2 cells, following the method of the previous example, in the presence or absence of the peptides used in the in vitro stimulation outlined supra, or SEQ ID NO: 1.

The results, presented in Figure 7 show that each culture exhibited a high level of specific lysis against both target cells pulsed with the testing peptide and with SEQ ID NO: 1.

Figure 7 also documents tumoricidal capacity of different cultures, by assessing this capacity against autologous Melan-A⁺ melanoma line Me 290. See example 1, supra. High tumoricidal activity was observed, with 50% maximal tumoricidal activity being observed at an effector/target ratio of 3:1 for the culture stimulated with SEQ ID NO: 2, 7:1 for that culture stimulated with SEQ ID NO: 1, 4:1 for that stimulated with SEQ ID NO: 17, 5:1 for that stimulated with SEQ ID NO: 13, and 15:1 for that stimulated with SEQ ID NO: 18.

EXAMPLE 19

Affinity of antigen recognition and relative antigenic activity of the different cell populations was then quantitated, using a standard CTL assay, along the lines of the assay of example 3, supra. Various ranges of peptide concentrations were used to develop titration curves, one of which is shown in Figure 8. These data are summarized in Table VII, which follows:

TABLE VII

Relative Potency of Melan-A Monospecific CTL Lines After Tetramer-Guided Fluorescent Cytometry Sorting.

Culture stimulated with SEQ ID NO:

(A)	2	1	17	13	18
Peptide [nM] 50%					
2	25	20	25	35	50
1	1	2.5	3	3	15
15	0.04	0.04	0.15	0.08	0.15
9	0.001	0.15	0.03	0.03	0.3
16	0.001	0.015	0.01	0.003	0.03

(B) Relative antigenic activity:					
2	1	1	1	1	1
1	25	8	8	12	3
15	625	500	166	437	333
9	25×10^3	133	833	1666	166
16	25×10^3	1333	2500	16×10^3	1666

(Values are the peptide concentration required for 50% maximal activity).

The affinity of the different lines for parental peptides was very similar, except for the line obtained after in vitro stimulation with SEQ ID NO: 18. This line was found to recognize complexes of HLA-A2/SEQ ID NO: 2 about 2 fold less efficiently, and complexes of HLA-A2/SEQ ID NO: 1, about 5 to 15 fold less efficiently than other cell lines.

With respect to the second part of Table VII it must be noted that regardless of the peptide used to stimulate expansion, all of the cell lines recognized complexes containing SEQ ID NO: 1 better than complexes containing SEQ ID NO: 2. Peptide analogues were recognized more efficiently than parental sequences by all lines, notwithstanding differences in relative

antigenicity for different lines. A preference of a cell line for an analogue did not always correlate with the analogue used to generate the cell line.

EXAMPLE 20

A series of plasmid constructs were prepared, which encoded either full length Melan-A, the peptide of SEQ ID NO: 1 ; the peptide of SEQ ID NO: 2; the peptide of SEQ ID NO: 13; or a variant of full length Melan-A, in which amino acid 27 (Ala), was replaced by Leu. These sequences were ligated into a plasmid construct known as the "Ubiquitin/Protein/Reference construct ("UPR" construct), as taught by Levy, et al., Proc. Natl. Acad. Sci USA 93:4907-4912 (1996), as well as in Valmori, et al., J. Exp. Med. 189(6):895-905 (1999), both of which are incorporated by reference. As described by Valmori, et al., supra, the plasmid is based on a commercially available plasmid, i.e., pS65T-C1, which carries, under the control of the CMV immediate early promoter, a mutated form of green fluorescence protein, which results in brighter fluorescence of the protein. Additionally, the stop codon of the sequence encoding this protein was replaced by a multicloning site which allows C terminal fusion to the protein. This is followed by a nucleic acid molecule which encodes yeast ubiquitin, with a mutation at position 48, changing Lys to Arg, to preclude the ability of the C-terminus of the ubiquitin encoding sequence to act as a ubiquitylation/degradation signal. Ubiquitin is a 76 amino acid polypeptide which, when fused to lysine residues in either monomeric or multimeric form often serves as a proteasomal degradation signal (see, e.g., Varshavsky, Trends Biochem. Sci 22:383-387 (1997)).

The UPR constructs contain sequences which encode linear fusion proteins which consist of ubiquitin flanked by the mutated form of the green fluorescence protein, or "GFP" described supra, and the protein of interest. The mutated form of GFP was followed by a peptide sequence derived from influenza hemagglutinin, which is recognized by a specific antibody. Specifically, the antibody was raised against peptide CYPYDVPDYASL (SEQ ID NO: 25), and is commercially available. The peptide sequence is referred to as "ha" hereafter, and is described by Ausubel, et al., Current Protocols in Molecular Biology (Wiley and Sons, 1992), and is incorporated by reference. The amino acid sequence of the "ha" fragment is YPYDVPDYA (SEQ ID NO: 26). Hence, the constructs can be referred to as "pGFP/Ub" or "GFPHaUbqX," where "X" is the molecule of interest. These constructs are useful because cleavage by ubiquitin

specific proteases following the last ubiquitin residue results in equimolar amounts of the protein of interest and the reference protein. See Levy, et al., Proc. Natl. Acad. Sci USA 93:4907-4912(1996), the disclosure of which is incorporated by reference. The system is also useful in that it permits one to generate minigene products without the need for a methionine residue at the N terminus. Hence, the relevant peptides can be generated directly.

The plasmid pGFP/Ub was treated with restriction endonucleases Sac II and Ava I. Then, either the open reading frame (ORF) for full length human Melan-A protein, a minigene encoding one of the peptides set forth supra, or a fragment which spanned the Melan-A ORF with the change at codon 27, were ligated into the plasmid. With respect to the minigenes, these were obtained by annealing complementary synthetic oligonucleotides which encoded the peptide, which had been designed to reconstitute the Sac II site at the 5' end, and the Ava I site at the 3' end, followed immediately by a stop codon. The fragment spanning the Melan-A ORF with a codon for alanine replacing one for leucine at position 27 was obtained by PCR amplification, using well known techniques. This last fragment was inserted between the BstEII and Ava I sites of the pGFP/Ub plasmid.

These constructs were then used to generate recombinant vaccinia viruses, as is detailed in the example which follows.

EXAMPLE 21

The five constructs discussed in example 20, supra, were digested with endonuclease BamHI, blunt ended using Klenow Pol I, and then digested further with Nhe I. This resulted in generation of DNA fragments which spanned the GFP-Ub and Melan-A encoding sequences.

These fragments were then isolated, and inserted into a plasmid which contains a mutated vaccinia virus promoter, i.e., promoter P7.5. This plasmid, referred to as pkT 1030, is described by Tsung, et al., J. Viral 70:165-171 (1996), incorporated by reference. The pkT 1030 plasmid was digested with Nhe I and Sma I, and then the fragments described supra were ligated into the plasmid, placing them under the control of the mutated promoter.

These recombinant plasmids were then digested with Hind III and Bgl II to produce cassettes which contained the fragment and the promoter. These cassettes were then ligated into

the Hind III and Bgl II sites of plasmid pkT 1401. This plasmid contains flanking sequences which are homologous to locus 14L of vaccinia.

Experiments were then carried out to recombine the relevant constructs into the 14L locus of vaccinia virus, using transient dominant gpt selection protocols on CV-1 cells (available from the American Type Culture Collection as ATCC CCL 70), and BSC-40 cells (which are a derivative of BSC-1 cells, available as ATCC CCL 26), following Zajac, Int. J. Canc 71:491-496 (1997), incorporated by reference. Recombinant plaques were purified, PCR screened, amplified, and semi purified on sucrose cushions. If necessary, viruses were inactivated using psoralen-long wave ultraviolet protocols, in accordance with Tsung, et al., J. Virol 70:165-171 (1996), incorporated by reference.

EXAMPLE 22

A human melanoma cell line, NA8-MEL, was used in these experiments. This cell line had been characterized previously as being HLA-A2 positive, and as one which does not express Melan-A antigen.

Samples of NA8-MEL cells were incubated for 1 hour at 37°C with Na⁵¹Cr, and were then infected with wild type vaccinia virus, recombinant vaccinia encoding full length Melan-A, or recombinant vaccinia encoding one of the three peptides described supra, at 10 MOI for 2 hours. Then, varying amounts of CTL line LAU 203EAA were combined with the labelled NA8-MEL cells, either with or without 1µM of the peptide of SEQ ID NO: 1. (The CTL line is polyclonal and monospecific). ⁵¹Cr release was measured after 4 hours of incubation at 37°C. Percent specific lysis was determined by subtracting spontaneous release of ⁵¹Cr from experimental release, dividing this figure by a value obtained by subtracting spontaneous release from total release, and multiplying the resulting fraction by 100.

Figure 9A depicts these results. After 2 hours of infection, cells infected with recombinant vaccinia encoding the complete Melan-A protein, peptide of SEQ ID NO: 1, or the peptide of SEQ ID NO: 2 showed low levels of lysis above background lysis secured using wild type vaccinia. In contrast, cells infected with recombinant virus expressing the peptide of SEQ ID NO: 13 showed efficient lysis, at levels comparable to those obtained using saturating amounts of exogenously added peptide SEQ ID NO: 1.

EXAMPLE 23

The low level of lysis obtained using the recombinant vaccinia virus encoding full length Melan-A might be a result of the short time period allowed for the assay, i.e., there may have been insufficient time for synthesis of sufficient fusion protein. In order to address this, NA8-
5 MEL cells were infected with recombinant virus as described supra, where the virus had been inactivated via psoralen-ultra violet light methodology. These conditions block viral replication, but early transcription proceeds, and persists longer than in cells infected with replicating virus, where early expression is inhibited rapidly. The cells were then cultured, overnight at 37°C, and then were tested as described, supra.

10 Overnight culture, however, did not result in improved CTL recognition, as is shown in figure 9B.

EXAMPLE 24

The experiments which follow were designed to determine the capacity of the recombinant vaccinia viruses described supra to induce Melan-A specific, tumor reactive CTL
15 responses.

First, a highly enriched CD8+ CTL preparation was obtained from an HLA-A*0201 positive melanoma patient, using magnetic cell sorting on the patient's PBMCs. The CD8+ population was then further selected, to obtain CD14+ cells. These CD14+ cells were used as the antigen presenting cells, or "APCs". These APCs were infected with recombinant viruses, using the same protocols as described supra. The cells were then washed extensively, and irradiated at 3000 rads. These irradiated cells were then mixed with the CD8+ cells referred to supra, at a 1:1 ratio, in 2 mls of medium supplemented with recombinant human IL-2 (100U/ml), and recombinant human IL-7 (10 ng/ml). As a control, CD8+ cells were stimulated with uninfected APCs alone, or APCs with the peptide of SEQ ID NO: 1 or SEQ ID NO: 13 at a concentration of 1 μM. Fourteen days after stimulation, the cultures were tested for presence of CD8+ cells which were positive for HLA-A2/Melan-A peptide tetramers. The tetramers are described, supra. These values were compared to the value obtained in testing freshly isolated CD8+ cells which were positive for the tetramer (0.08%).

There was no significant variance in the frequency of specific CD8+ cells in the absence of antigen specific stimulation, nor was there an increased frequency when the antigen presenting cells were infected with recombinant vaccinia viruses encoding the complete Melan-A protein or the peptides. In contrast the mutant "A27L" form of Melan-A resulted in a 115 fold increase in stimulation, which was superior to the increase observed using SEQ ID NO: 1 (38 fold increase), and similar to that obtained using SEQ ID NO: 13 (125 fold increase).

5 This pattern was repeated when PBMCs from additional melanoma patient were tested, although the absolute values were somewhat different.

EXAMPLE 25

10 Additional experiments were carried out to document the ability of Melan-A specific CTLs which had been obtained by stimulation with the recombinant vaccinia viruses to specifically recognize Melan-A expressing melanoma cells. In these experiments, the CD8+ T cells obtained following the stimulation were cocultured (2×10^5 CD8+ T cells) with either NA8-MEL cells, or HLA-A2 positive, Melan-A positive Me290 cells. The ratio of effector: 15 target cells used was 2:1. Cells were placed in 96 well round bottom microplates in 200 μ l of RPMI-10% fetal calf serum, containing 200U/ml of recombinant human IL-2. The cells were incubated, overnight, at 37°C, and IFN- γ production was then measured, using an ELISA, as described by Elsasser-Beile, et al., J. Immunol Meth 139:191-195 (1991).

20 No IFN- γ above background levels was released by any of the cultures when NA8-MEL was used; however, significant amounts of IFN- γ were produced by the cultures with Me290. Further, the level of IFN- γ correlated directly with the percentage of A2/Melan-A tetramer positive cells in the culture.

EXAMPLE 26

25 These experiments were designed to evaluate the impact in vivo of enhanced stimulatory capacity of recombinant vaccinia viruses which contain a minigene that encodes the peptide of SEQ ID NO: 13. Transgenic A2/Kb mice (2-3 months old) were immunized, intraperitoneally, with 10^7 pfus of recombinant vaccinia virus encoding the peptide of SEQ ID NO: 1 , SEQ ID NO:13, and a peptide consisting of amino acids 271-279 of MAGE-3 (SEQ ID NO: 21).

Specifically, the construct described by Valmori, et al., J. Exp. Med. 189(6): 895-905 (1999), incorporated by reference, was used. This construct was treated with restriction endonucleases to produce a fragment similar to fragments described supra, in that it contained a coding sequence for GFP-Ub-MAGE-3 peptide. The fragment was then treated with restriction endonuclease BamHI, blunt ended with Klenow Pol I, and digested further with Nhe I. The resulting fragment was inserted into the Nhe I/Sma I site of Vaccinia vector. The resulting, recombinant Vaccinia vector was then used in the same way the other recombinant vectors described herein were used. Three weeks later, mice were sacrificed, and single cell suspensions were prepared from their spleens. T cells were purified by passage on nylon wool columns. Then 2×10^6 purified T cells were cultured with 2×10^5 irradiated (10000 rads) EL-4 A2/Kb cells (EL-4 cells which had been transfected with an HLA-A*0201/Kb gene) which had been pulsed with $1 \mu\text{M}$ of the peptide of SEQ ID NO: 13 previously (1 hour at 37°C , in 12 well cell culture plates in 2ml of DMEM medium supplemented with 10mM HEPES, $50 \mu\text{M}$ β 2-mercaptoethanol, 10% FCS, and EL-4 cell culture supernatant with 30U/ml of IL-2). As a control, nylon purified T cells isolated from the spleen of naive mice were used.

The T cells from the mice immunized with vaccinia virus encoding SEQ ID NO: 1 exhibited low to undetectable peptide specific CTL activity after two rounds of in vitro stimulation, which was similar to the results obtained with the mice that had been immunized with the vaccinia virus encoding MAGE-3 and the naive mice; however, high levels of peptide specific lysis were detected for the cells obtained from mice that had been immunized with the vaccinia virus encoding SEQ ID NO: 13.

EXAMPLE 27

The experiments set forth supra show that a single mutation was important in determining immunogenicity of the vaccinia viruses. These experiments were designed to determine the impact of introducing the A27L mutation into a full gene, rather than the minigene.

The construct which encodes Melan-A A27L mutant is described, supra. NA8-MEL cells were plated in 96 well plates, together with 200 ng of plasmid DNA, and $1 \mu\text{l}$ lipofectamine, in a final volume of $100 \mu\text{l}$ of DMEM medium. The materials were cultured for 6 hours at 37°C . Then, $100 \mu\text{l}$ of DMEM medium containing 10% FCS was added to each well, and the cells were

maintained at 37°C for an additional 14 hours. Following this, transfected cells were tested for their ability to stimulate release of TNF- α by a Melan-A specific CTL line. In brief, CTLs were added to the target, or stimulator cells in 100 μ l of Iscove's medium, supplemented with 10% human serum, and 20U/ml recombinant human IL-2. After 24 hours of incubation at 37°C, supernatants were collected, and TNF- α content was determined, in a functional assay, using WEHI-164 clone 13, as described by Espevik, et al., J. Immunol Meth 95: 99-105 (1986), and Hansen, et al., J. Immunol Meth 119: 203-210 (1989).

The results are in accordance with results secured using the peptides per se. In other words, vectors which encoded peptides which have been shown to have enhanced activity, when used, showed more efficient T cell lysis than vectors which encoded peptides known to have lower activity. The higher activity levels may be attributed to the known, improved binding ability of the mutant peptide. Hence, one aspect of the invention is the development of expression vectors, vaccinia vectors in particular, which encode peptides which bind to MHC molecules. Preferably, there are peptides which, when bound to an MHC molecule, provoke lysis of cells which present the complexes by cytolytic T cells. More preferably, these vectors encode peptides of nine or ten amino acids which are identical to known MHC binding peptides but for mutations at the N terminal, or second amino acid. Such mutations have enhanced binding properties, as was shown supra. It is well within the skill of the artisan to first identify a nona- or decapeptide which binds to an MHC molecule, and preferably stimulates CTL activity, and then to create variants of these peptides, with changes at the first or second position of the sequence. Basic information regarding the codons corresponding to the replacement amino acids can be used to create the relevant expression vectors.

The foregoing examples, as will be seen, describe the various features of the invention. These include peptides which bind to HLA molecules, such as HLA-A2 molecules, exemplified by HLA-A*0201, which may also provoke proliferation of cytolytic T cells, preferably with concomitant provocation of effector function(s). These peptides, as will be seen from the data herein, are nonapeptides or decapeptides. As with all peptides, the first amino acid is the amino terminus, and the last one is the carboxy terminus. The peptides of the invention may be decapeptides, which have a Val moiety at the C, or carboxy terminus. They may have Tyr or Phe at the amino terminus when the second amino acid is Ala. In another embodiment, the amino

terminus is Glu followed by Ala, Leu or Met in the second and third position, and the C terminus is Val, wherein if position two is Ala, position three must be Met or Leu, and vice versa. The peptides having the amino acid sequences set forth in any of SEQ ID NOS: 6, 7, 9 and 12-15 are exemplary.

5 Also a part of the invention are isolated cytolytic T cell lines which are specific for complexes of these peptides and their MHC binding partner, i.e., an HLA molecule, such as an HLA-A2 molecule, HLA-A*0201 being especially preferred.

10 The ability of these peptides to bind to HLA molecules makes them useful as agents for determining presence of HLA-A2 positive cells, such as HLA-A*0201 positive cells, by determining whether or not the peptides bind to cells in a sample. This "ligand/receptor" type of reaction is well known in the art, and various methodologies are available for determining it.

15 A further aspect of the invention are so-called "mini genes" which carry information necessary to direct synthesis of modified decapeptides via cells into which the mini genes are transfected. Mini genes can be designed which encode one or more antigenic peptides, and are then transferred to host cell genomes via transfection with plasmids, or via cloning into vaccinia or adenoviruses. See, e.g., Zajac, et al., Int. J. Cancer 71: 496 (1997), incorporated by reference. These recombinant vectors, such as recombinant vaccinia virus vectors, can be constructed so as to produce fusion proteins. For example, as was shown, supra, fusion proteins can be constructed where one portion of the fusion protein is the desired tumor rejection antigen precursor, or tumor rejection antigen, and additional protein or peptide segments can be included. Exemplary, but by no means the only types of additional protein or peptide segments which can be added to the fusion proteins, are reporter proteins or peptides, i.e., proteins or peptides which give an observable signal so as to indicate that expression has occurred, such as green fluorescence protein. Additional reporter proteins include, but are by no means limited to, proteins such as β galactosidase, luciferase, dhfr, and "eGFP", or enhanced green fluorescent protein, as described by Cheng, et al., Nature Biotechnology 14:606 (1996), incorporated by reference, and so forth. The various reporter proteins available to the skilled artisan can be, and are used, in different ways. For example, "GFP" and "eGFP" can be used to visualize infected cells, thereby facilitating tracking when flow cytometry is used, and the isolation of the cells so infected. Other reporter proteins are useful when methods such as western blotting,

immunoprecipitation, and so forth are used. These techniques are standard in the art and need not be reiterated here. Protein or peptide segments which facilitate the cleavage of the tumor rejection antigen precursor or tumor rejection antigen from the fusion peptide may also be included. The fusion protein can include more than one tumor rejection antigen, as described, supra, and can also include proteins or peptides which facilitate the delivery of the tumor rejection antigen or antigens to a relevant MHC molecule. Such proteins and peptides are well known to the art, and need not be elaborated herein.

Also a part of the invention are recombinant cells which have been transfected with the recombinant reporter vectors described herein. Such cells may be, e.g., any type of eukaryotic cell, with human cells being especially preferred. Such cells can then be used, e.g., to produce tumor rejection antigen precursors or tumor rejection antigens. They can also be used, in an ex vivo context, to generate cytolytic T cells specific for particular complexes of MHC molecules and tumor rejection antigens. This can be done simply by contacting the transfected cells to a source of T cells, such as a blood sample, so as to provoke the proliferation of any cells in the sample specific to the complexes of MHC molecules and TRAs (i.e., tumor rejection antigens) produced following expression of the fusion protein, and processing of the TRA. Such cells, when rendered non-proliferative, can also be used as vaccine materials, as they will present the relevant complexes on their surface, and provoke the same type of T cell response in vivo, as is shown herein. Similarly, the vectors can be used as vaccine materials per se, and can be administered to a patient in need of a T cell response against complexes of MHC molecules and peptide on cell surfaces. Of course, T cells generated ex vivo can also be used to treat patients.

The peptides may be combined with peptides from other tumor rejection antigens to form 'polytopes'. Exemplary peptides include those listed in U.S. Patent Application Serial Numbers 08/672,351, 08/718,964, now U.S. Patent No. _____, 08/487,135 now U.S. Patent No. _____, 08/530,569 and 08/880,963 all of which are incorporated by reference.

Additional peptides which can be used are those described in the following references, all of which are incorporated by reference: U.S. Patent Nos. 5,405,940; 5,487,974; 5,519,117; 5,530,096; 5,554,506; 5,554,724; 5,558,995; 5,585,461; 5,589,334; 5,648,226; and 5,683,886; PCT International Publication Nos. 92/20356; 94/14459; 96/10577; 96/21673; 97/10837; 97/26535; and 97/31017 as well as pending U.S. Application Serial No. 08/713,354.

Polytope are groups of two or more potentially immunogenic or immune stimulating peptides, which can be joined together in various ways, to determine if this type of molecule will stimulate and/or provoke an immune response.

These peptides can be joined together directly, or via the use of flanking sequences. See 5 Thompson et al., Proc. Natl. Acad. Sci. USA 92(13): 5845-5849 (1995), teaching the direct linkage of relevant epitopic sequences. The use of polytope as vaccines is well known. See, e.g., Gilbert et al., Nat. Biotechnol. 15(12): 1280-1284 (1997); Thomson et al., supra; Thomson et al., J. Immunol. 157(2): 822-826 (1996); Tam et al., J. Exp. Med. 171(1): 299-306 (1990), all of which are incorporated by reference. The Tam reference in particular shows that polytope, 10 when used in a mouse model, are useful in generating both antibody and protective immunity. Further, the reference shows that the polytope, when digested, yield peptides which can be and are presented by MHCs. Tam shows this by showing recognition of individual epitopes processed from polytope 'strings' via CTLs. This approach can be used, e.g., in determining how many epitopes can be joined in a polytope and still provoke recognition and also to 15 determine the efficacy of different combinations of epitopes. Different combinations may be 'tailor-made' for the patients expressing particular subsets of tumor rejection antigens. These polytope can be introduced as polypeptide structures, or via the use of nucleic acid delivery systems. To elaborate, the art has many different ways available to introduce DNA encoding an individual epitope, or a polytope such as is discussed supra. See, e.g., Allsopp et al., Eur. J. 20 Immunol. 26(8): 1951-1959 (1996), incorporated by reference. Adenovirus, pox-virus, Ty-virus like particles, plasmids, bacteria, etc., can be used. One can test these systems in mouse models to determine which system seems most appropriate for a given, parallel situation in humans. They can also be tested in human clinical trials.

Also, a feature of the invention is the use of these peptides to determine the presence of 25 cytolytic T cells in a sample. It was shown, supra, that CTLs in a sample will react with peptide/MHC complexes. Hence, if one knows that CTLs are in a sample, HLA-A2 positive cells can be "lysed" by adding the peptides of the invention to HLA-A2 positive cells, such as HLA-A*0201 positive cells, and then determining, e.g., radioactive chromium release, TNF production, etc. or any other of the methods by which T cell activity is determined. Similarly, 30 one can determine whether or not specific tumor infiltrating lymphocytes ("TILs") are present

in a sample, by adding one of the claimed peptides with HLA-A2 positive cells to a sample, and determining lysis of the HLA-A2 positive cells via, e.g., ^{51}Cr release, TNF presence and so forth. In addition, CTL may be detected by ELISPOT analysis. See for example Schmittel et al., (1997). J. Immunol. Methods 210: 167-174 and Lalvani et al., (1997). J. Exp. Med. 126: 859 or by FACS analysis of fluorogenic tetramer complexes of MHC Class I/peptide (Dunbar et al., (1998), Current Biology 8: 413-416, Romero, et al., J. Exp. Med. 188: 1641-1650 (1998). All are incorporated by reference.

Of course, the peptides may also be used to provoke production of CTLs. As was shown, supra, CTL precursors develop into CTLs when confronted with appropriate complexes. By causing such a "confrontation" as it were, one may generate CTLs. This is useful in an in vivo context, as well as ex vivo, for generating such CTLs.

Other features of the invention will be clear to the skilled artisan, and need not be repeated here.

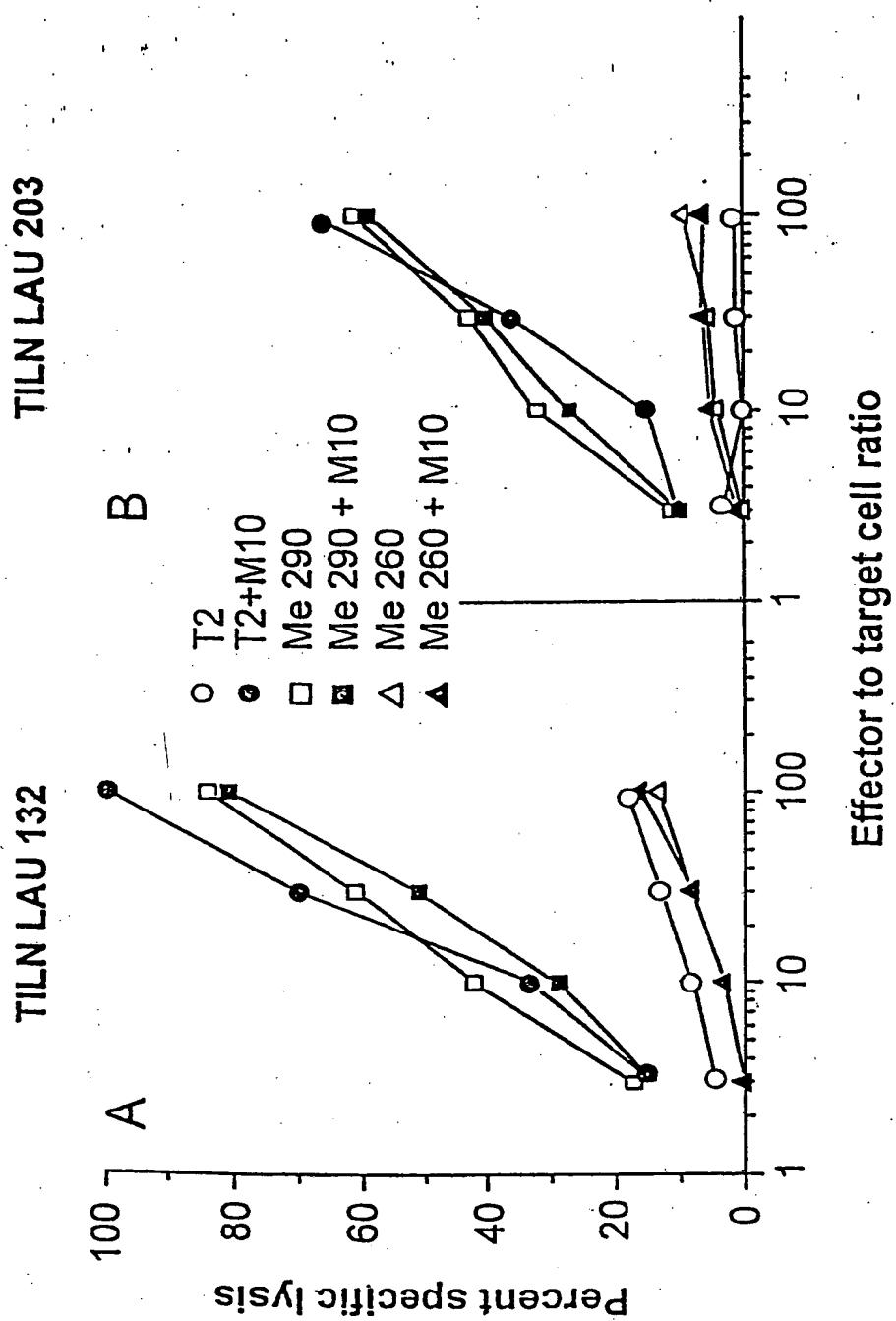
The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, it being recognized that various modifications are possible within the scope of the invention.

WE CLAIM:

1. A recombinant vaccinia reporter vector which expresses a fusion protein molecules comprising (i) a reporter protein and (ii) (a) at least one tumor rejection antigen, or (b) a tumor rejection antigen precursor, or (c) a tumor rejection antigen precursor said recombinant vaccinia reporter vector comprising a nucleic acid molecule which encodes said fusion protein, in operable linkage with a promoter.
2. The recombinant vaccinia vector of claim 1, wherein said reporter protein comprises green fluorescence protein.
3. The recombinant vaccinia vector of claim 1, wherein said reporter protein comprises ubiquitin.
4. The recombinant vaccinia vector of claim 1, wherein said reporter protein comprises green fluorescence protein and ubiquitin.
5. The recombinant vaccinia vector of claim 1, wherein said fusion protein comprises a tumor rejection antigen.
6. The recombinant vaccinia vector of claim 1, wherein said fusion protein comprises a plurality of tumor rejection antigens.
7. The recombinant vaccinia vector of claim 1, wherein said fusion protein comprises a tumor rejection antigen precursor.
8. Recombinant cell comprising the recombinant vaccinia virus of claim 1.
9. A method for provoking a cytolytic T cell specific for an MHC molecule and a tumor rejection antigen, comprising transfecting a cell which presents said MHC molecule on

its surface with the recombinant vaccinia virus vector of claim 1, wherein said recombinant vaccinia virus vector expresses a fusion protein comprising a tumor rejection antigen, culturing said cell under condition favoring cleavage of said tumor rejection antigen from said fusion protein and formation of complexes between said tumor rejection antigen and said MHC molecule, and contacting said cell to a T cell containing sample to provoke proliferation of cytolytic T cells specific for said complexes.

10. The method of claim 9, wherein said MHC molecule is an HLA-A2 molecule.
11. A method for treating a patient suffering from a disorder characterized by presentation of complexes of an MHC molecule and a tumor rejection antigen on cell surfaces, comprising administering an amount of the recombinant vaccinia virus vector of claim 1 to said patient in an amount sufficient to be processed by cells which present said complexes on their surfaces to tumor rejection antigens, and proliferation of native cytolytic T cells which lyse said cells.
12. A method for treating a patient suffering from a disorder characterized by presentation of complexes of an MHC molecule and a tumor rejection antigen on their surfaces, comprising administering to said patient an amount of cytolytic T cells produced by contacting the recombinant cell of claim 8 to a sample containing T cells ex vivo, sufficient to lyse cells which present said complexes on their surface.
13. A method for treating a patient suffering from a disorder characterized by presentation of complexes of an MHC molecule and a tumor rejection antigen on their surfaces, comprising administering to said subject an amount of the recombinant cell of claim 8, which has been rendered non-proliferative, in an amount sufficient to provoke cytolytic T cells specific to said complexes.

Figure 1**SUBSTITUTE SHEET (RULE 26)**

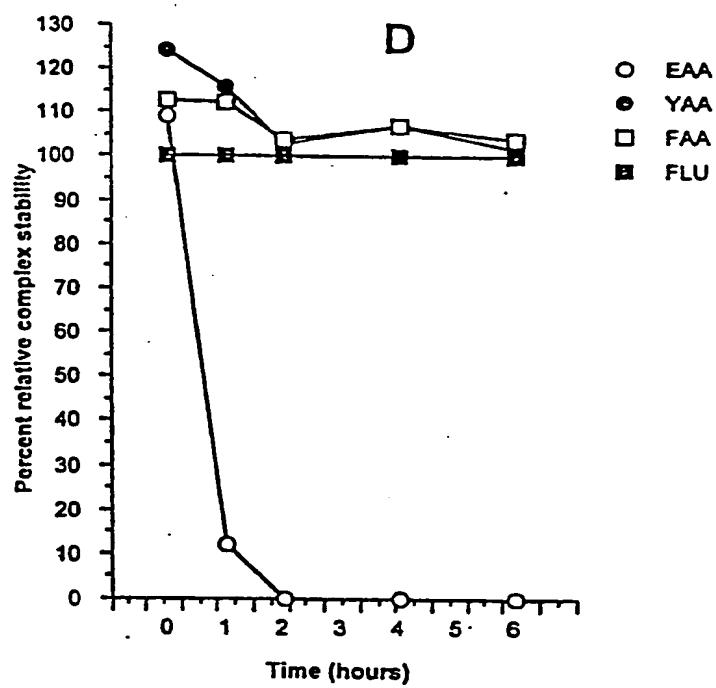
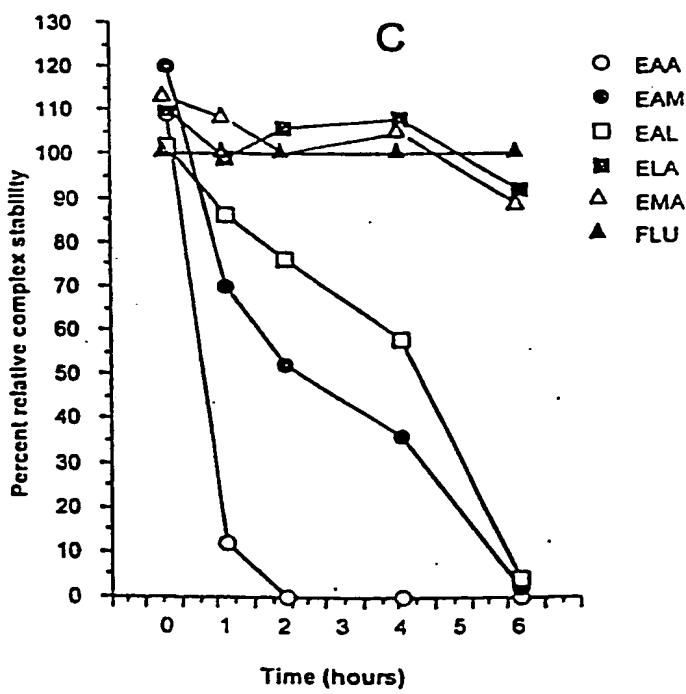
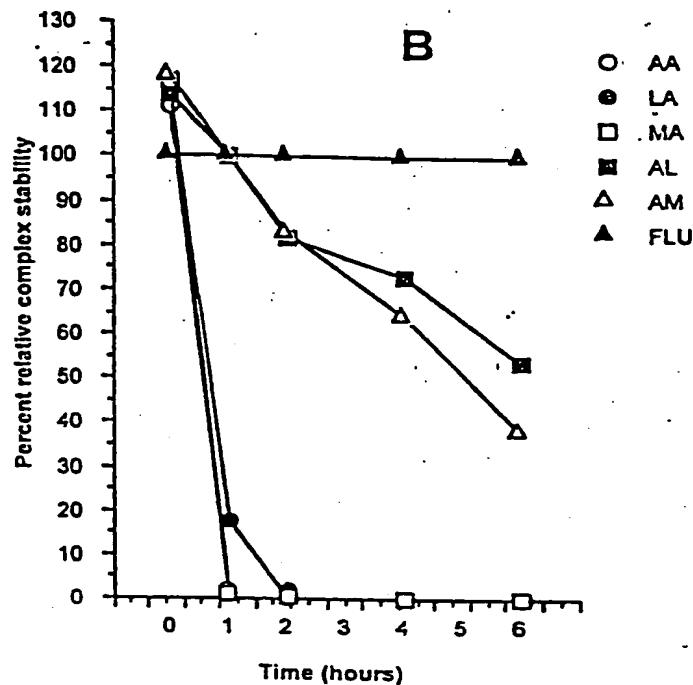
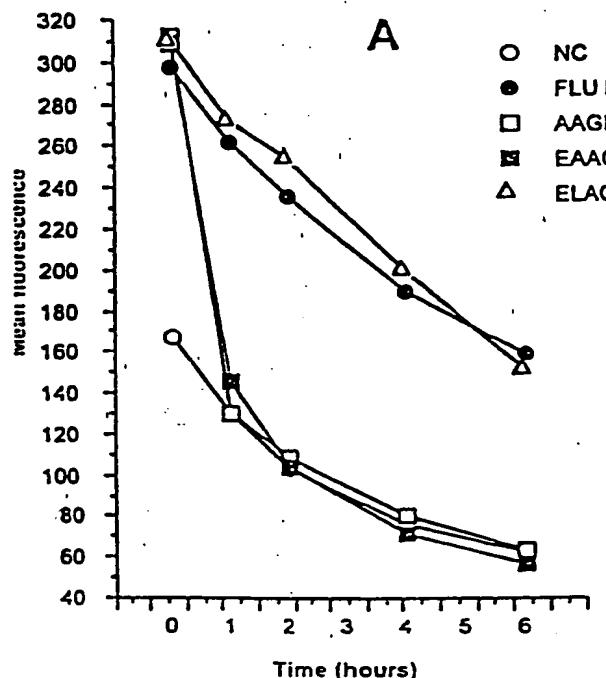


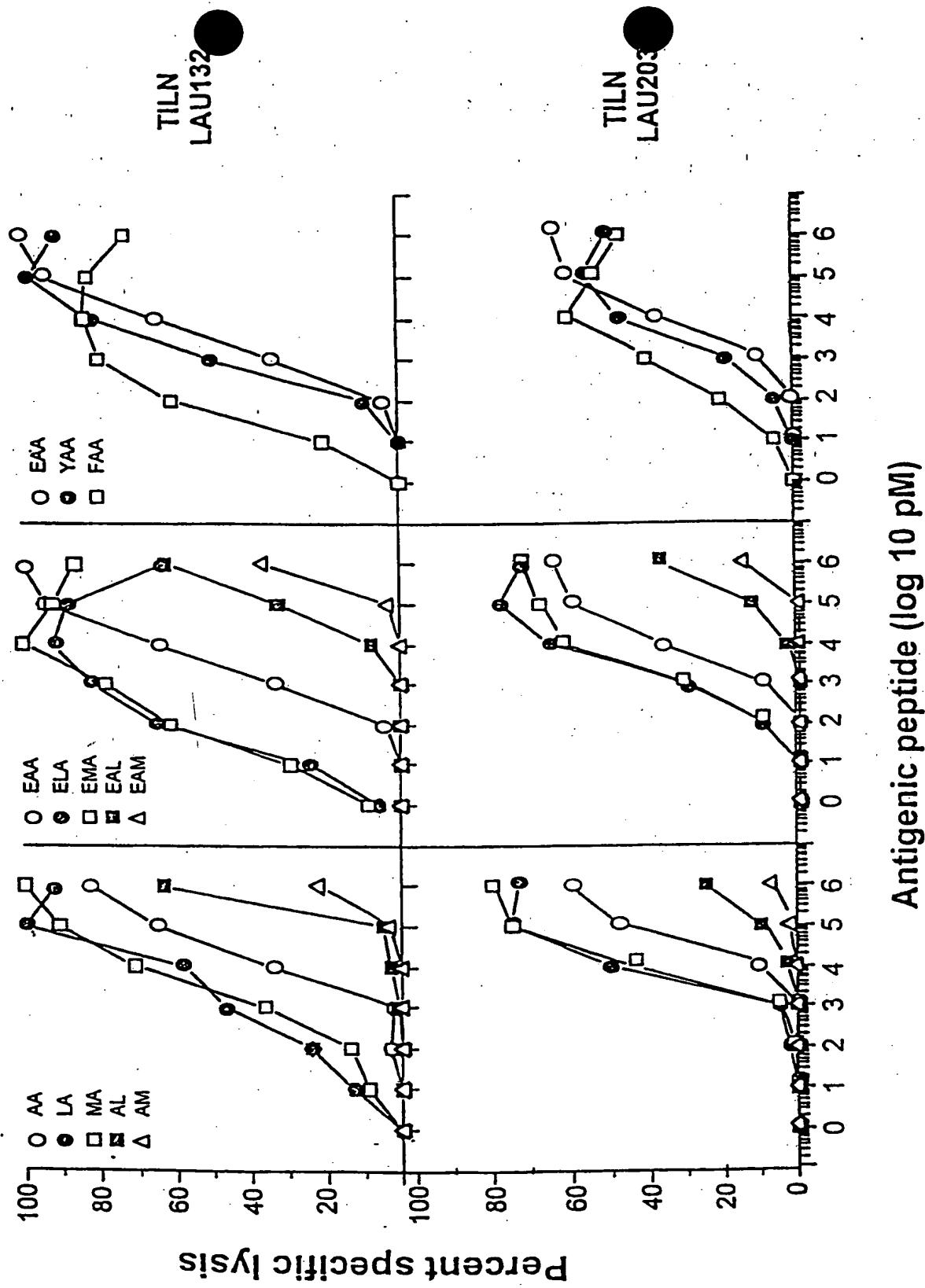
Figure 3**SUBSTITUTE SHEET (RULE 26)**

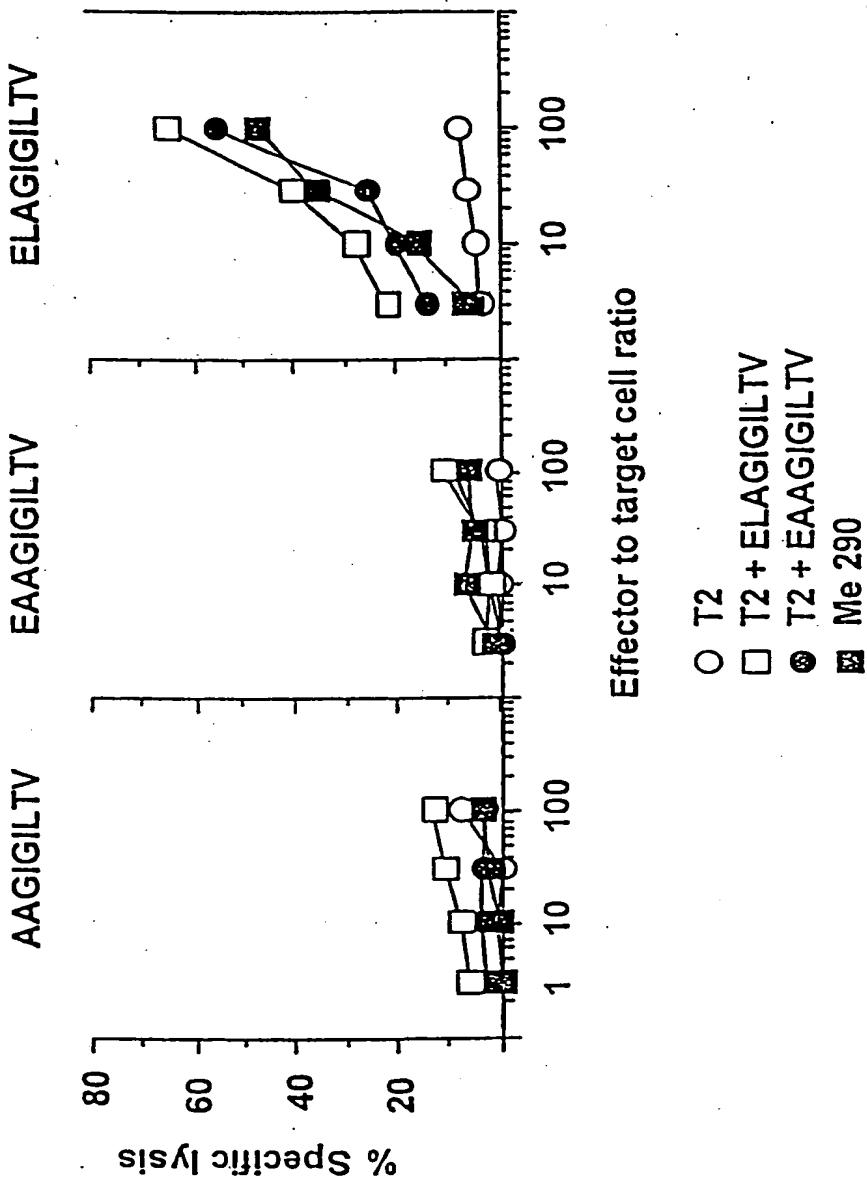
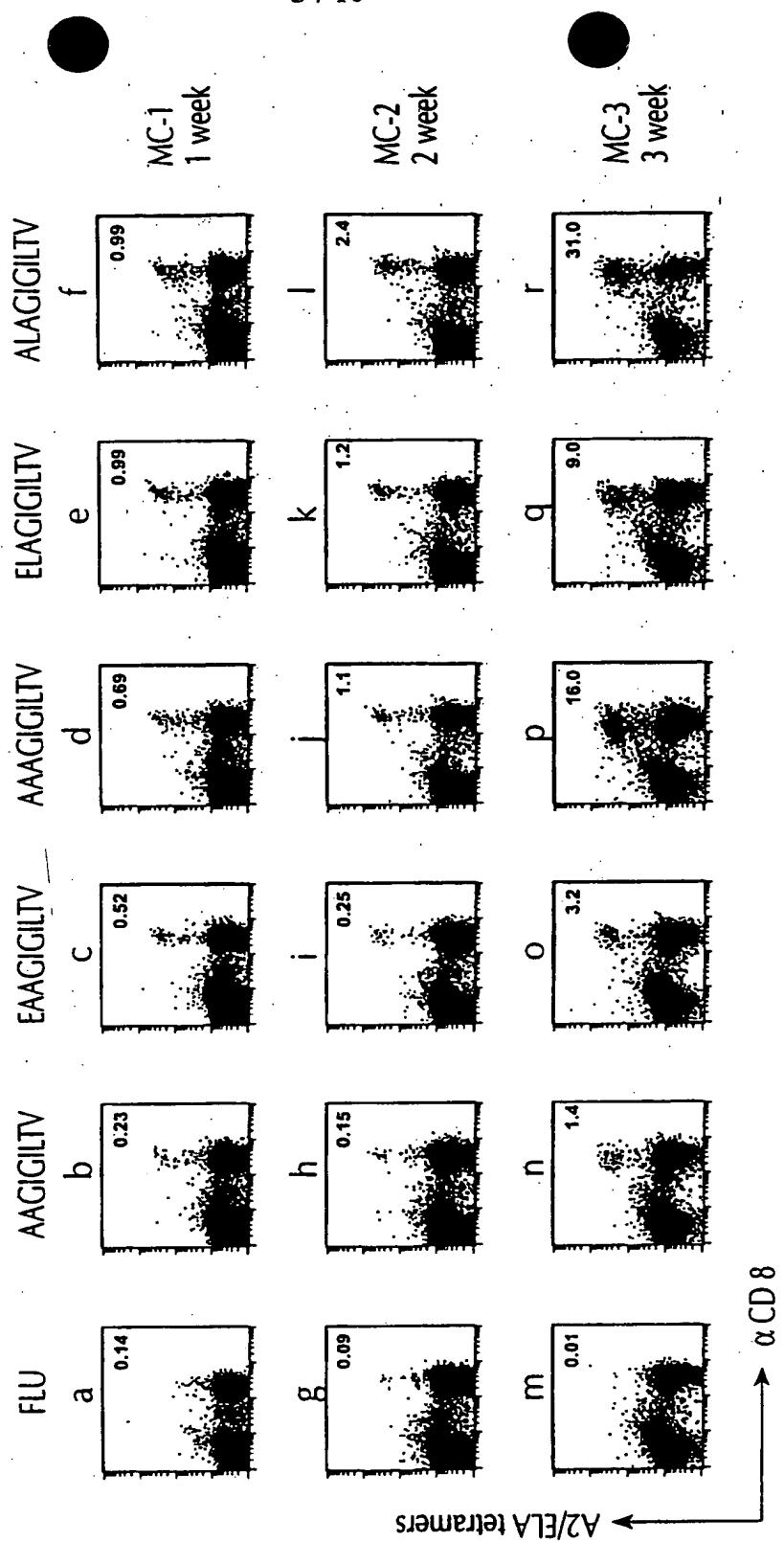
Figure 4**Induction of Melan-A specific, tumor reactive
CTL by *in vitro* stimulation with Melan-A peptide analogs**

FIG. 5



SUBSTITUTE SHEET (RULE 26)

Figure 6

Assay of lytic activity of PBMC from a melanoma patient after three rounds of in vitro stimulation with Melan-A derived peptides.

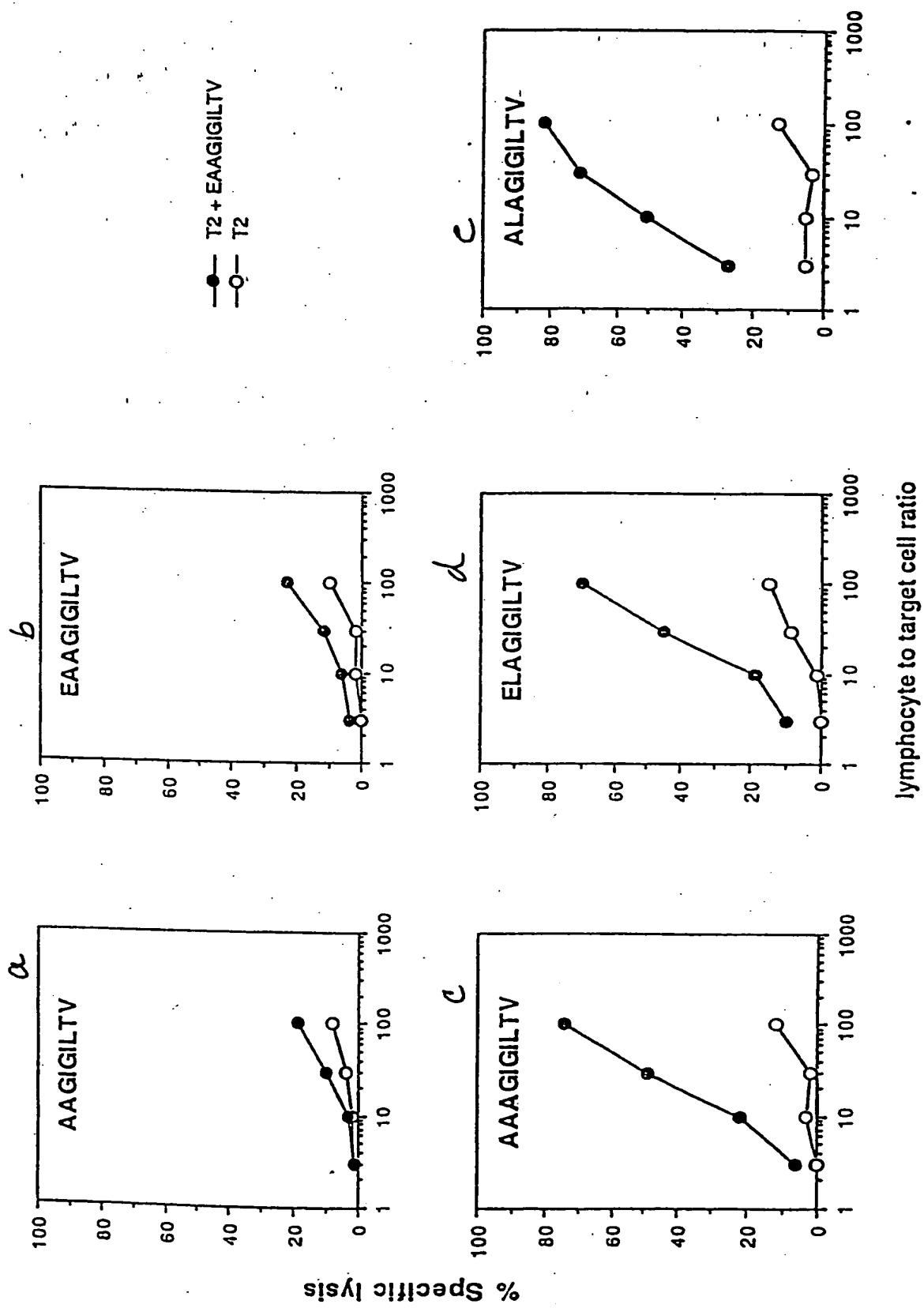
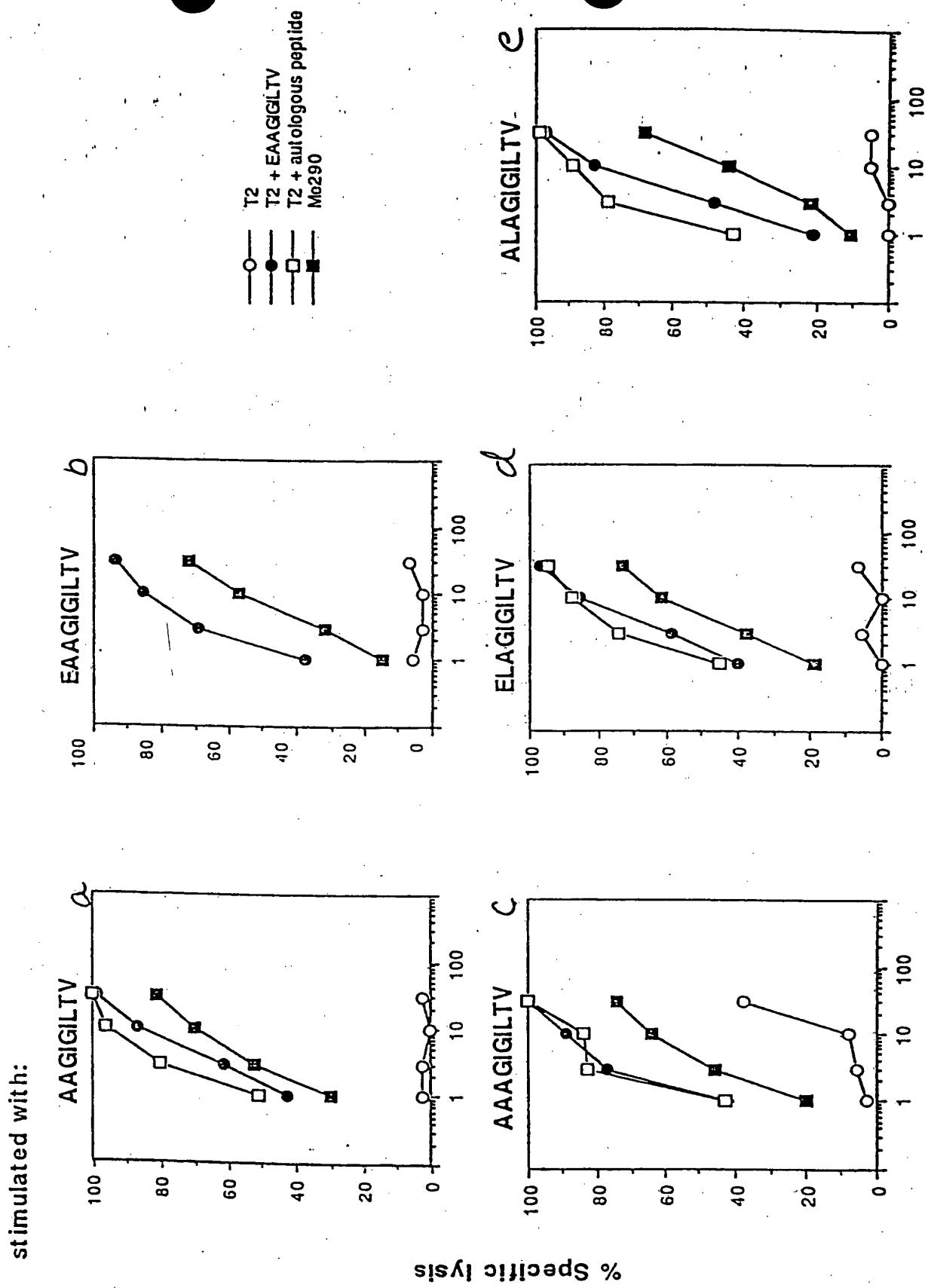


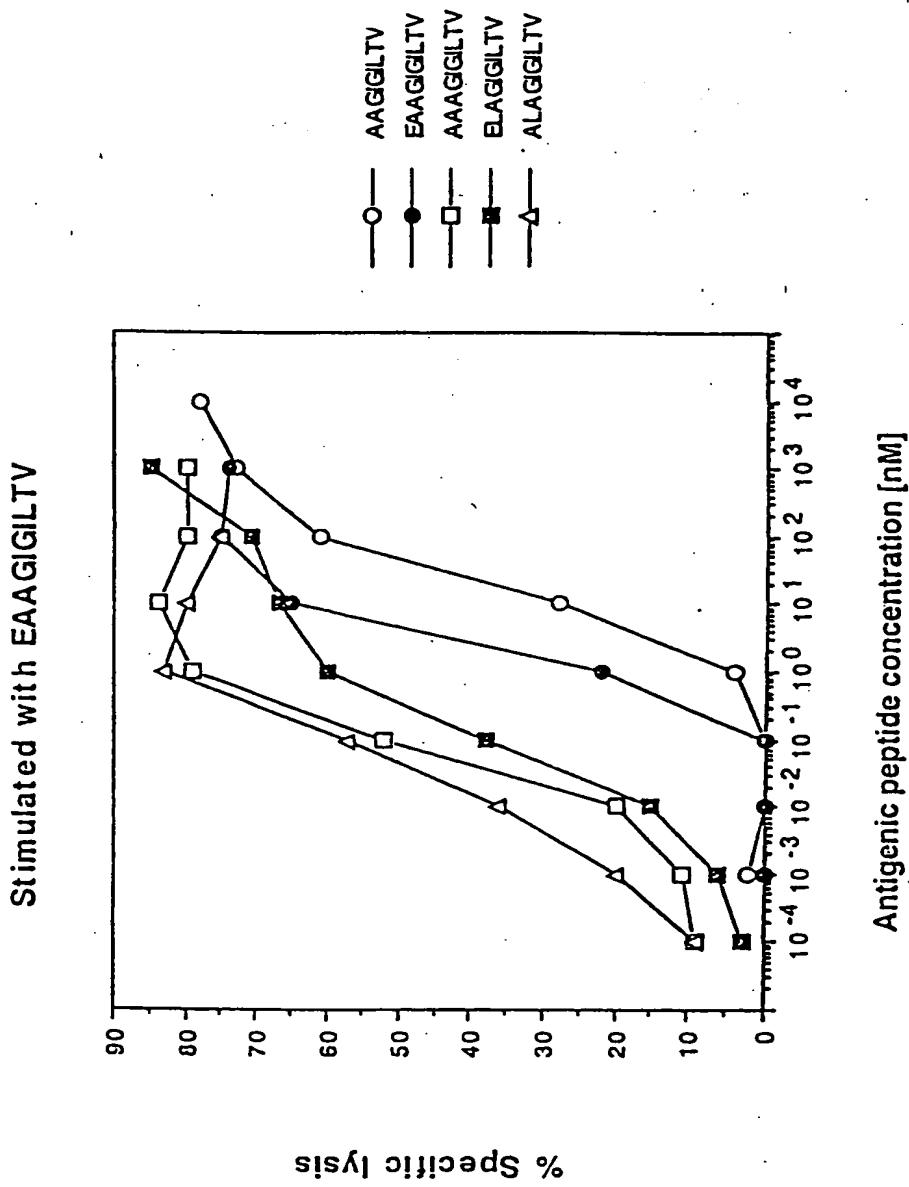
Figure 7
Melan-A specific lytic activity of fluorescently sorted tetramer⁺ lymphocytes



SUBSTITUTE SHEET (RULE 26)

Figure 8

Quantitative assessment of the peptide-dependent lytic activity of a Melan-A specific CTL line rendered monospecific by tetramer-guided fluorescent cell sorting.

**SUBSTITUTE SHEET (RULE 26)**

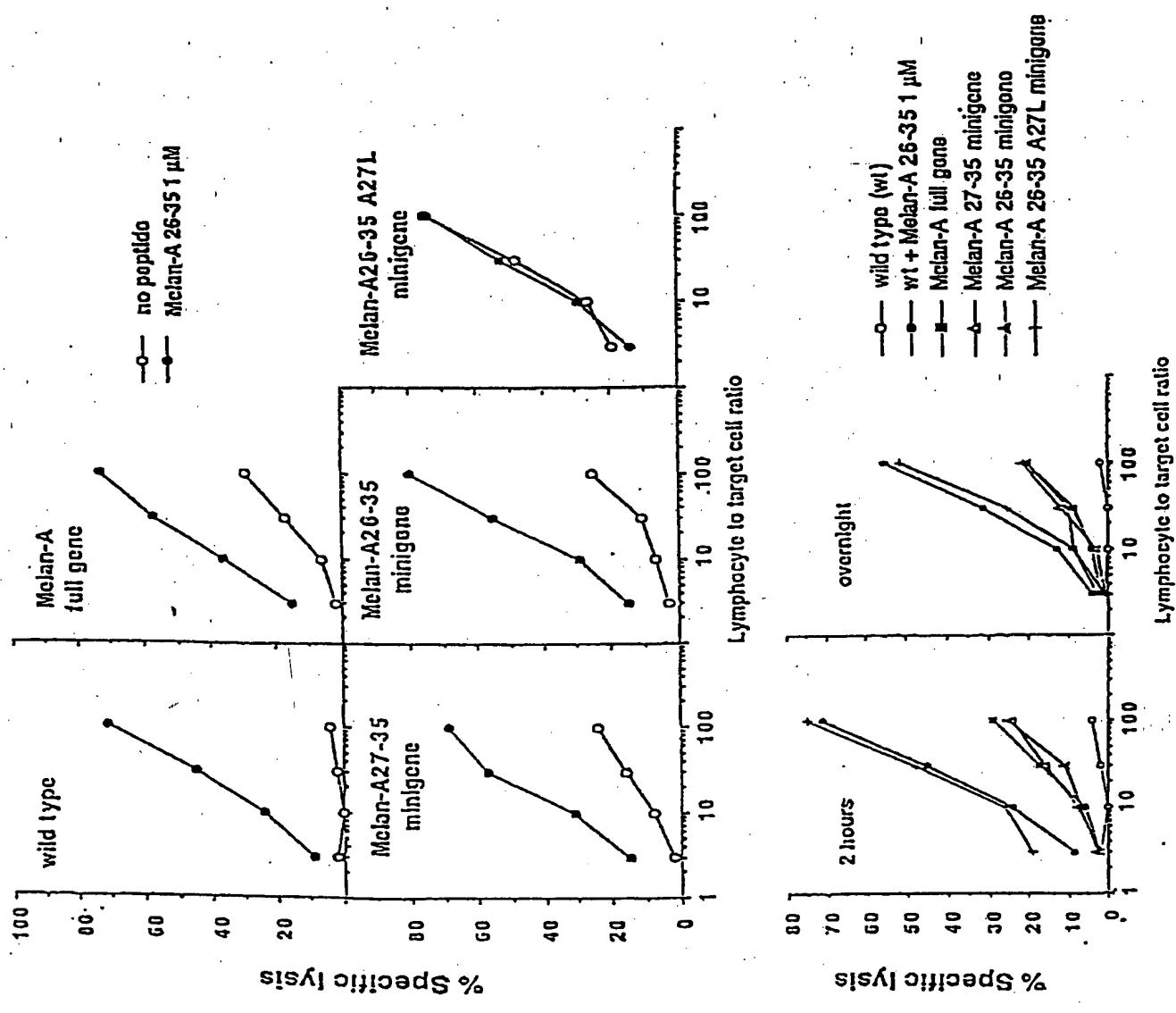
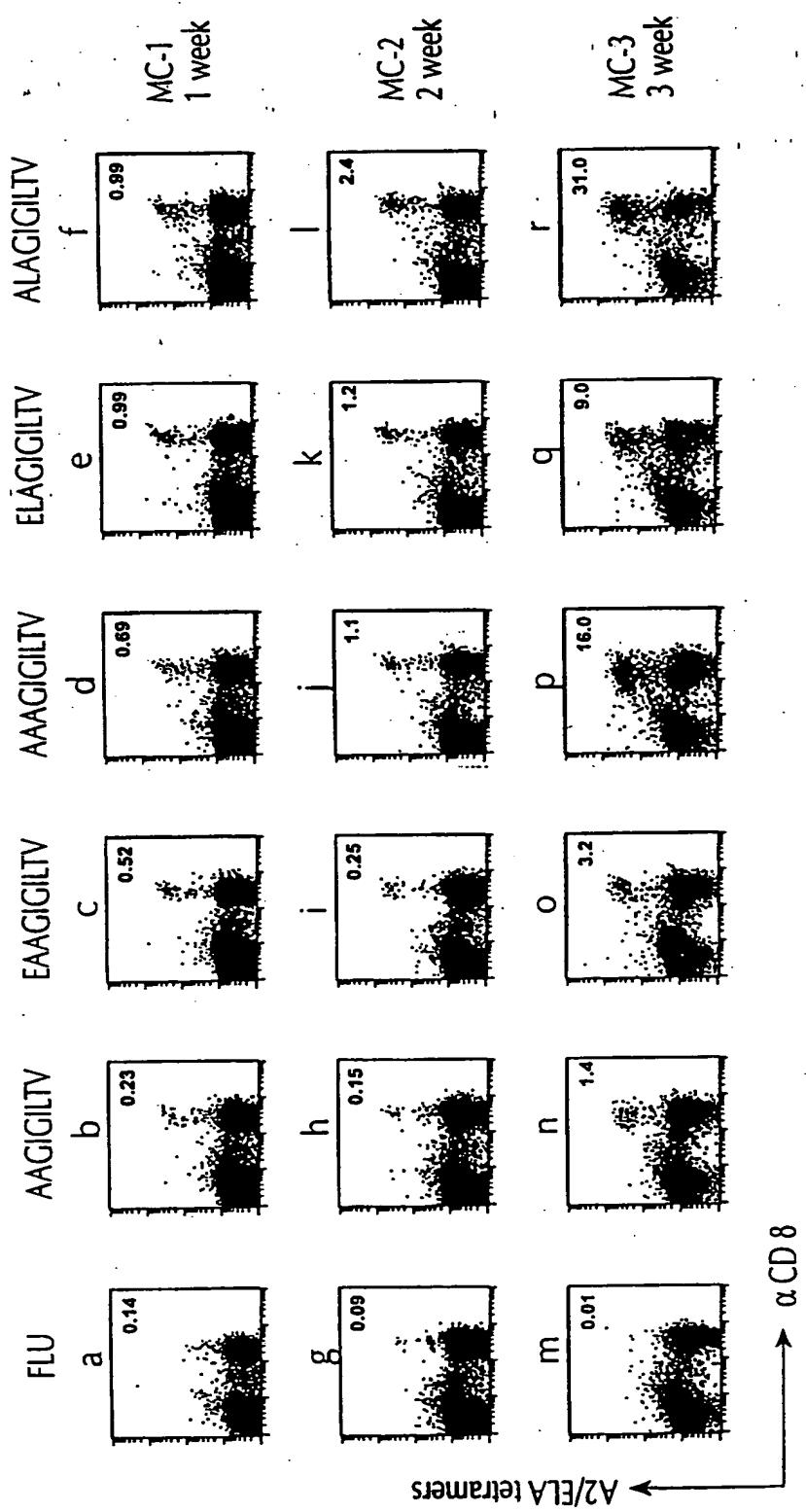


Figure 9

SUBSTITUTE SHEET (RULE 26)

FIG. 5



SUBSTITUTE SHEET (RULE 26)

<110> Valmori, Danila
Levy, Frederic
Miconnet, Isabelle
Cerottini, Jean-Charles
Romero, Pedro
<120> Isolated Nona - And Decapeptides Which Bind
To HLA Molecules, and the Use Thereof
<130> LUD 5608
<140> US09/386,581
<141> 1999-08-30
<150> US09/099,543
<151> 1998-06-18
<150> US 09/061,388
<151> 1998-04-16
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<223>Portion of Influenza A matrix protein

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<223> Peptide from protein MAGE-3

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<223> Mutant Ras 5-14 Peptide

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INTERNATIONAL SEARCH REPORT

Inte. Application No
PCT/US 00/23536

A. CLASSIFICATION OF SUBJECT MATTER	IPC 7 C12N15/12 C07K14/47 C12N15/863 C12N15/62 A61K31/70	A61K35/14
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According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

-Minimum documentation searched (classification system followed by classification symbols)
IPC 7 C12N C07K A61K

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

EPO-Internal

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	VALMORI D ET AL: "MODULATION OF PROTEASOMAL ACTIVITY REQUIRED FOR THE GENERATION OF ACYTOTOXIC T LYMPHOCYTE-DEFINED PEPTIDE DERIVED FROM THE TUMOR ANTIGEN MAGE-3" JOURNAL OF EXPERIMENTAL MEDICINE, TOKYO, JP, vol. 189, no. 6, 15 March 1999 (1999-03-15), pages 895-905, XP000925674 ISSN: 0022-1007 cited in the application the whole document ---	1-8
Y	WO 98 15638 A (LUDWIG INST CANCER RES) 16 April 1998 (1998-04-16) page 6, line 2 -page 9, line 25; claims 1,7,9,10,20,23,25 page 16, paragraph 2 ---	1-13 -/-

Further documents are listed in the continuation of box C.

Patent family members are listed in annex.

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Date of the actual completion of the international search

1 December 2000

Date of mailing of the international search report

07/12/2000

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Authorized officer

Smalt, R

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/23536

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No:
Y	WO 98 58951 A (LUDWIG INST CANCER RES) 30 December 1998 (1998-12-30) page 28, line 21 -page 29, line 8; claims 7,8	1-10
Y	WO 99 37771 A (HOON DAVID S B ;WAYNE JOHN CANCER INST (US)) 29 July 1999 (1999-07-29) the whole document	1,3,5, 8-13
A	WO 96 10419 A (US HEALTH) 11 April 1996 (1996-04-11) page 17, paragraph 3 - paragraph 4 page 19, last paragraph; claims 20,21	1,8,11, 12
P,X	VALMORI D ET AL: "Induction of potent antitumor CTL responses by recombinant vaccinia encoding a Melan-A peptide analogue" JOURNAL OF IMMUNOLOGY, US, THE WILLIAMS AND WILKINS CO. BALTIMORE, vol. 164, no. 2, 2000, pages 1125-1131, XP002139351 ISSN: 0022-1767 the whole document	1-13

INTERNATIONAL SEARCH REPORT

Information on patent family members

International application No

PCT/US2000/23536

Patent document cited in search report		Publication date	Patent family member(s)		Publication date
WO 9815638	A	16-04-1998	AU	4668797 A	05-05-1998
WO 9858951	A	30-12-1998	US	6025470 A	15-02-2000
			AU	7982798 A	04-01-1999
			CN	1261374 T	26-07-2000
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			JP	10506902 T	07-07-1998

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